

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 24, 2003, 11:50:09 ; Search time 38 Seconds  
(without alignments)  
981.847 Million cell updates/sec

Title: US-09-993-420A-3

Perfect score: 1479  
Sequence: 1 MTRCTADNSLTNPATRRRTM.....ACATGIVGVYCGRMFLSK 280

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: A\_Geneseq\_101002:\*  
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
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8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*  
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*  
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*  
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12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*  
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14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*  
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*  
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19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1476	99.8	280	15	AAAR7343
2	161.5	10.9	192	20	AAAY05533
3	151	10.2	192	20	AAW97393
4	151	10.2	193	19	AAW61391
5	151	10.2	193	20	AAAY05531
6	151	10.2	193	20	AAW97391
7	150	10.1	193	20	AAAY05530
8	148	10.0	192	20	AAW97394
9	148	10.0	193	18	AAW6047
10	148	10.0	193	19	AAW61392

11	148	10.0	193	20	AAAY05532	Human Bcl-w protei
12	148	10.0	193	20	AAW97392	The human bcl-y pr
13	145.5	9.8	168	18	AAW6048	Mouse bcl-w protei
14	138	9.3	233	22	AAW73304	Mutant rat Bcl-XL
15	136	9.2	225	18	AAU00219	Bcl-XL-DTR apoptos
16	135.5	9.2	225	18	AAW0396	"Deprenyl" (RTM)-1
17	135	9.1	233	16	AAW6887	Human thymus Bcl-X
18	135	9.1	233	17	AAW05821	Bcl-XL protein. H
19	135	9.1	233	18	AAW31530	Human anti-apoptot
20	135	9.1	233	21	AAW83223	Bcl-x polypeptide.
21	135	9.1	233	21	AAW69969	Human Bcl-XL prote
22	135	9.1	233	22	AAW64262	Human Bcl-XL prote
23	135	9.1	233	22	AAW73303	Rat wild-type Bcl-
24	135	9.1	233	22	AAW50538	Human Bcl-XL prote
25	135	9.1	233	22	AAW47515	Protein encoded by
26	126.5	8.6	212	22	AAW64285	Mutant bcl-xl prot
27	126	8.5	365	19	AAW5884	Amino acid sequenc
28	120.5	8.1	232	17	AAW01019	Apoptosis-blocking
29	120.5	8.1	232	20	AAW94346	Human Bcl-2 mutant
30	119.5	8.1	232	17	AAW01020	Apoptosis-blocking
31	119.5	8.1	232	20	AAW94347	Human Bcl-2 mutant
32	118.5	8.0	236	22	AAW35131	Murine Bcl-2. Mus
33	118.5	8.0	236	22	AAW76554	Murine Bcl-2 polyp
34	117.5	7.9	485	22	AAU00222	Lfn-Bcl-XL apoptos
35	117	7.9	239	20	AAW01018	Apoptosis-blocking
36	117	7.9	239	20	AAW94345	Human Bcl-2 wild-t
37	116	7.8	239	20	AAW87810	Human Bcl-2. Homo
38	116	7.8	239	22	AAW74127	Human bcl-2. Homo
39	116	7.8	239	22	AAW48288	Human Bcl-2. Homo
40	116	7.8	239	22	AAW35130	Human Bcl-2. Homo
41	116	7.8	239	22	AAW50537	Human Bcl-2 protei
42	116	7.8	239	23	AAU76553	Human Bcl-2 polype
43	115	7.8	239	15	AAW47344	Human oncogene bcl
44	115	7.8	239	17	AAW02383	Human BCL2. Homo
45	114.5	7.7	212	22	AAW20495	Human Bcl-XL (tran

#### ALIGNMENTS

RESULT 1	
AAAR7343	
ID	AAAR7343 standard; Protein; 280 AA.
XX	
AC	AAAR7343;
XX	
DT	23-JUN-1994 (first entry)
XX	
DE	ced-9 protein.
XX	
KW	Cell death; senescence; programmed cell death; ced-9; myocardial
KW	infarction; stroke; brain injury; neurodegenerative disease;
KW	muscular degenerative disease; ageing; hypoxia; ischaemia; toxemia;
KW	infection; hair loss; neoplasia; cancer; ced-3; ced-4; bcl-2;
KW	oncogene.
XX	
OS	Caenorhabditis elegans.
XX	
PN	W09325683-A.
XX	
PD	23-DEC-1993.
XX	
PF	14-JUN-1993; 93MO-US05651.
XX	
PR	12-JUN-1992; 92US-0898933.
XX	
PA	10-AUG-1992; 92US-0927681.
XX	
PI	(MAST) MASSACHUSETTS INST TECHNOLOGY.
XX	
DR	Hengartner M, Horvitz HR;
XX	
DR	WPI; 1994-007540/01.
DR	N-PSDB; AA054630.

XX Caenorhabditis elegans cell death-protective gene - used to  
 PT develop agents for preventing cell death or for reducing  
 PT population of cells  
 XX  
 PS Claim 5; Page 59-60; 112pp; English.  
 XX  
 CC ced-9 is essential for C. elegans development and apparently  
 CC functions by protecting cells during development from programmed  
 CC cell death. ced-9 was shown to function by antagonising the  
 CC activities of cell death genes ced-3 and ced-4. The protein product  
 CC of the human oncogene bcl-2 was found to have a similar sequence  
 CC to the ced-9 protein. The ced-9 gene can be used for developing  
 CC agents for treating a condition characterised by increased cell death  
 CC such as myocardial infarction, stroke, traumatic brain injury,  
 CC neurodegenerative disease, muscular degenerative disease, ageing,  
 CC hypoxia, ischaemia, toxemia, infection or hair loss. It can also  
 CC be used for reducing a population of cells in the treatment of  
 CC neoplastic growth cancerous tissue, infected cells or autoreactive  
 CC immune cells.  
 XX  
 SQ Sequence 280 AA;  
 Query Match 99.8%; Score 1476; DB 15; Length 280;  
 Best Local Similarity 99.6%; Pred. No. 5.3e-160;  
 Matches 279; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDEGINSADADLPSPRQASTRRM 60  
 DB 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDEGINSADADLPSPRQASTRRM 60  
 QY 61 SIGESIDGKINDMEERPLDIEGFVDFYTHIRIQNGEMFGARGLPCGVQPEHEMRVWG 120  
 DB 61 SIGESIDGKINDMEERPLDIEGFVDFYTHIRIQNGEMFGARGLPCGVQPEHEMRVWG 120  
 QY 121 TIEFKKAENPTEPCBELLAVPRISFLYQDVVRTVGNADTDCPMSTYGLIGLISFGGG 180  
 DB 121 TIEFKKAENPTEPCBELLAVPRISFLYQDVVRTVGNADTDCPMSTYGLIGLISFGGG 180  
 QY 181 VAAKMMSEVELQGVNRLFVYTSLEFKTRIRNNMKEHNRSWDDFMTLGKMKEDYERAE 240  
 DB 181 VAAKMMSEVELQGVNRLFVYTSLEFKTRIRNNMKEHNRSWDDFMTLGKMKEDYERAE 240  
 QY 241 EKYGRKRNRRMSIGAGVTAIGIYGVVCGRRMFSLK 280  
 DB 241 EKYGRKRNRRMSIGAGVTAIGIYGVVCGRRMFSLK 280  
 RESULT 2  
 ID AAY05533 standard; Protein; 192 AA.  
 XX  
 AC AAY05533;  
 XX  
 DT 05-JUL-1999 (first entry)  
 XX  
 DE Mouse Bcl-w protein derivative.  
 XX  
 KW Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;  
 KW animal model.  
 XX  
 OS Mus sp.  
 XX  
 PN W09913710-A1.  
 XX  
 PD 25-MAR-1999.  
 XX  
 PF 16-SEP-1998; 98WO-AU00764.  
 XX  
 PR 16-SEP-1997; 97AU-0009228.  
 XX  
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
 XX

PI Adams J, Cory S, Gibson L, Koentgen F, Print C;  
 XX  
 DR WPI; 1999-243890/20.  
 DR N-PSDB; AAX25135.  
 XX  
 PT An animal model exhibiting reduced levels of a Bcl-w protein and/or  
 PT protein associated with Bcl-w  
 XX  
 PS Disclosure; Page 39; 52pp; English.  
 XX  
 CC The present sequence is described of a derivative of mouse Bcl-w  
 CC (see also AAY0531), a pro-survival member of the Bcl-2 family that  
 CC is widely expressed and which is essential for spermatogenesis.  
 CC The derivative lacks the 24 N-terminal amino acids of Bcl-w.  
 CC The invention relates generally to a method of treatment and to an  
 CC animal model for the identification of molecules and genetic  
 CC sequences useful for inducing or reducing fertility of male animals.  
 CC Methods are provided for the treatment of infertility, or for  
 CC reducing fertility, by modulating spermatogenesis. An animal model  
 CC carries a mutation is at least one allele of the human or murine  
 CC bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w.  
 CC Such animals have disorganised seminiferous tubules and are  
 CC substantially infertile, but possess no other major abnormalities  
 CC as determined by histological examination. They can be used to  
 CC screen for therapeutic molecules including genetic sequences  
 CC capable of inducing, enhancing or otherwise facilitating  
 CC spermatogenesis in animals, or which can induce infertility.  
 XX  
 SQ Sequence 192 AA;  
 Query Match 10.9%; Score 161.5; DB 20; Length 192;  
 Best Local Similarity 25.6%; Pred. No. 8.1e-10;  
 Matches 54; Conservative 29; Mismatches 89; Indels 39; Gaps 8;  
 QY 79 DIEGFVDFYTHIRIQNGEMFGARGLPCGVQPEHEMRVWGTFIEKKHAENPTEPCBOL 138  
 DB 9 DTRALVADPVGTRLNQKGYCGAGBEPADPLQANRAAGDEFETFRRTFSDLAOL 68  
 QY 139 IAVP-----RISFLYQDVVRTVGNADTDCPMSTYGLIGLISFGFVAARM--ES 188  
 DB 69 HTVPSAQORFQVSDLEFG-----GPNNGRIAVAFVFGAALCAESVNM 115  
 QY 189 VELQGVNRLFVYTSLEFKTRIRNNMKEHNRSWDDFMTL-GKMKEDYERAEKVRK 247  
 DB 116 EPLVQVQDWIV--AYLETRLA-DWHSQGMADFTALYDGALED-----AKRL 162  
 QY 248 ONRRMSIGAGVTAIGIYGVVCGRRMFS 278  
 DB 163 REGNNAV--STVYTGAVAGALVYGAFFAS 191  
 RESULT 3  
 ID AAM97393  
 XX  
 AC AAM97393 standard; Protein; 192 AA.  
 XX  
 DT 20-MAY-1999 (first entry)  
 XX  
 DE Protein sequence of the specification.  
 XX  
 KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;  
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
 KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;  
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;  
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
 KW premature cell death; cell death stimulator; prolonged cell life span;  
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;  
 KW parasite.  
 KW  
 OS Unidentified.  
 XX  
 PN US5883229-A.

Query Match	Similarity	10.2%	Score 151;	DB 20;	Length 192;
Best Local	Similarity	24.3%	Pred. No. 1.3e-08;		
Matches	51;	Conservative	31;	Mismatches	92;
				Indels	36;
				Gaps	

  

Qy	79	DIEGEVYDFTIRIRONGENMFAGPGLPCGCVQDEHEHMAKMTIFPKKAENFETICEQL	138
		: : : : :   : : : : :   : : : : :   : : : : :   : : : : :	
Db	8	DTRALVADVYGLKLRKRGVCGAGPEGPADPLHOAMRAADGETFTRRRFTTSDLAOL	67
		: : : : :   : : : : :   : : : : :   : : : : :   : : : : :	
Qy	139	LAVP-----RISFSLQDVVTRTGMNQTDQCPMSYGLTIGLISFGGFVAKKM--ES	188
		: : : : :   : : : : :   : : : : :   : : : : :   : : : : :	
Db	68	HTPGSAQGRFTFQVSDLELQG-----GPNMGSLVAFVFGAALCAESYNNKE	114
		: : : : :   : : : : :   : : : : :   : : : : :   : : : : :	
Qy	189	VELQGVQRRLFYVTSLEFTRIRNNKKEHNRSWDDYMTLGKQMKKEYERAEAKVRRRQ	248
		: : : : :   : : : : :   : : : : :   : : : : :   : : : : :	
Db	115	EPYVGQVQPMV--TYLLETRLA-DWISSGGAAEFTAL-----YGDQALEE-ARRLL	162
		: : : : :   : : : : :   : : : : :   : : : : :   : : : : :	
Qy	249	NRRSMIGAGVTGAGIGVGVVCGRMFS	278
		: : : : :   : : : : :   : : : : :   : : : : :   : : : : :	
Db	163	EGMNASVRT-VLTGVALGALVTVGAFFAS	191
		: : : : :   : : : : :   : : : : :   : : : : :   : : : : :	

  

RESULT 4
AAW61391
ID AAW61391 standard; Protein; 193 AA.
AAW61391;
AAW61391;
AC
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HO
HP
HQ

[illegible]







Db 68 HVTGSAQQRFTQVSDLEFG-----GNMGRIVAFVFGALCAESVNRKM 114  
 QY 189 VELGGOVRLNFVYTSLEIKTRIRNNKHEHNSWDDEMTLGKQKEDYERAEKVRGRKQ 248  
 Db 115 EPLVGQVQEMWV---AVLETRLA-DWIHSSGMAEFETAL-----YGDGALDEE-ARRLR 162  
 QY 249 NRRMSMIGAGVTAGAIGIVGVCGRRMFS 278  
 Db 163 EGNMASVVRT-VLTGAVALGALVTGAFEPAS 191

RESULT 9  
 AAM36047  
 ID AAM36047 standard; Protein; 193 AA.

XX AC AAM36047;  
 XX DT 22-APR-1998 (first entry)  
 XX DE Human bcl-2 protein.  
 XX KM Bcl-2; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;  
 XX KM diagnosis; degenerative disease.  
 XX OS Homo sapiens.  
 XX PN MO9735971-A1.  
 XX PD 02-OCT-1997.  
 XX PE 27-MAR-1997; 97WO-AU00199.  
 XX PR 27-MAR-1996; 96AU-0008965.  
 XX PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
 XX PI Adams JM, Cory S, Gibson LM, Holmgren SP;  
 XX DR WPI; 1997-489635/45.  
 XX DR N-PSDB; AAT96577.  
 XX PT Nucleic acid encoding apoptosis related gene bcl-2 - used to induce  
 XX PT or inhibit cell survival, e.g. for treatment of cancer and  
 XX PT degenerative diseases  
 XX PS Claim 6; Page 48; 86pp; English.

CC This sequence represents a novel human protein, bcl-2, encoded by the  
 CC bcl-2 gene family and extracted from an adult brain library. This gene  
 CC promotes cell survival, so its modulation is useful in treatment of  
 CC cancer or auto-immune diseases, degenerative diseases (e.g. stroke,  
 CC Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia,  
 CC ischemia, human immunodeficiency virus infection or in cell transplants.  
 CC up-regulation of the gene can also be used to modify cell lines cultured  
 CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas  
 CC and to increase survival of primary explants during genetic modification.  
 CC It can be used to produce recombinant Bcl-2 for therapy, diagnosis,  
 CC antibody production or screening of potential modulators.

XX Sequence 193 AA;

Query Match 10.0%; Score 148; DB 18; Length 193;  
 Best Local Similarity 24.3%; Pred. No. 2,9e-08;  
 Matches 51; Conservative 30; Mismatches 93; Indels 36; Gaps 8;

QY 79 DIEGFVVDYFTIRIRONGMEWFGAPGLPCGVQPEHEMNRVMTIFEKKAENFETFEOL 138  
 Db 9 DTRALVADFEVGYKLRQKGYCGAGPEGPADPLHOAMRAAGDEFEFRFRFSDLAOL 68  
 QY 139 LAVP-----RISFSLYQDVVTRVGNAGTQCPMSYGRLLIGLSFGFVAKKM--ES 188  
 Db 69 HVTGSAQQRFTQVSDLEFG-----GNMGRIVAFVFGALCAESVNRKM 115

QY 189 VELGGOVRLNFVYTSLEIKTRIRNNKHEHNSWDDEMTLGKQKEDYERAEKVRGRKQ 248  
 Db 116 EPLVGQVQEMWV---AVLETRLA-DWIHSSGMAEFETAL-----YGDGALDEE-ARRLR 163  
 QY 249 NRRMSMIGAGVTAGAIGIVGVCGRRMFS 278  
 Db 164 EGNMASVVRT-VLTGAVALGALVTGAFEPAS 192

RESULT 10  
 AAM61392  
 ID AAM61392 standard; Protein; 193 AA.

XX AC AAM61392;  
 XX DT 02-OCT-1998 (first entry)  
 XX DE Human bcl-2 protein.  
 XX KM bcl-2; bcl-2; cell death pathway; apoptotic; apoptosis; human.  
 XX OS Homo sapiens.  
 XX PN US5789201-A.  
 XX PD 04-AUG-1998.  
 XX PE 11-FEB-1997; 97US-0798897.  
 XX PR 23-FEB-1996; 96US-0012201.  
 XX PR 11-FEB-1997; 97US-0798897.  
 XX PA (COCE-) COCENSYS INC.  
 XX PI Guastella J;  
 XX DR WPI; 1998-446079/38.  
 XX DR N-PSDB; AAV28334.  
 XX PT Nucleic acids encoding B-cell lymphoma-2 protein - useful for  
 XX PT producing recombinant protein for use in treating uncontrolled cell  
 XX PT growth e.g. cancers  
 XX PS Example; Column 17/18; 27pp; English.

CC The mammalian bcl-2 protein is a member of the bcl-2 family, components  
 CC in the cell death pathway. The bcl-2 family have both apoptotic activity  
 CC and the apoptosis blocking activity. bcl-2 fails in the apoptosis  
 CC activity category. The recombinant protein may be used to prevent  
 CC uncontrolled cell growth, either by its direct administration to  
 CC recombinant genetic constructs to increase its expression in vivo. Also,  
 CC antisense constructs can be used in disorders where prevention of cell  
 CC death is desired.

XX Sequence 193 AA;

Query Match 10.0%; Score 148; DB 19; Length 193;  
 Best Local Similarity 24.3%; Pred. No. 2,9e-08;  
 Matches 51; Conservative 30; Mismatches 93; Indels 36; Gaps 8;

QY 79 DIEGFVVDYFTIRIRONGMEWFGAPGLPCGVQPEHEMNRVMTIFEKKAENFETFEOL 138  
 Db 9 DTRALVADFEVGYKLRQKGYCGAGPEGPADPLHOAMRAAGDEFEFRFRFSDLAOL 68  
 QY 139 LAVP-----RISFSLYQDVVTRVGNAGTQCPMSYGRLLIGLSFGFVAKKM--ES 188  
 Db 69 HVTGSAQQRFTQVSDLEFG-----GNMGRIVAFVFGALCAESVNRKM 115  
 QY 189 VELGGOVRLNFVYTSLEIKTRIRNNKHEHNSWDDEMTLGKQKEDYERAEKVRGRKQ 248  
 Db 116 EPLVGQVQEMWV---AVLETRLA-DWIHSSGMAEFETAL-----YGDGALDEE-ARRLR 163

QY 249 NRKSMIGAGYTAGAIGIVGVCGRMFS 278  
 DB 164 EGNMASVRT-VLTGAVALGALVTGAFEPAS 192

## RESULT 11

AAV05532  
 ID AAV05532 standard; Protein; 193 AA.

AC AAV05532;

DT 05-JUL-1999 (first entry)

DE Human Bcl-w protein essential for spermatogenesis.

KW Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;  
 animal model.

XX Homo sapiens.

PN W09913710-A1.

PD 25-MAR-1999.

PE 16-SEP-1998; 98MO-AU00764.

PR 16-SEP-1997; 97AU-0009228.

PA (HALT-) HALT INST MEDICAL RES WALTER & ELIZA.

PI Adams J, Cory S, Gibson L, Koenigen F, Print C;

DR WPI: 1999-243890/20.

DR N-PSDB: AAX25134.

PT An animal model exhibiting reduced levels of a Bcl-w protein and/or  
 protein associated with Bcl-w

PS Disclosure; Page 37; 52pp; English.

XX The present sequence is described of a derivative of human Bcl-w  
 (see also AAY05530), a pro-survival member of the Bcl-2 family that  
 is widely expressed and which is essential for spermatogenesis.  
 CC The invention relates generally to a method of treatment and to an  
 animal model for the identification of molecules and genetic  
 CC sequences useful for inducing or reducing fertility of male animals.  
 CC Methods are provided for the treatment of infertility, or for  
 CC reducing fertility, by modulating spermatogenesis. An animal model  
 CC carries a mutation is at least one allele of the human or murine  
 CC bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w.  
 CC Such animals have disorganised seminiferous tubules and are  
 CC substantially infertile, but possess no other major abnormalities  
 CC as determined by histological examination. They can be used to  
 CC screen for therapeutic molecules including genetic sequences  
 CC capable of inducing, enhancing or otherwise facilitating  
 CC spermatogenesis in animals, or which can induce infertility.

XX Sequence 193 AA;

Query Match 10.0%; Score 148; DB 20; Length 193;

Best Local Similarity 24.3%; Pred. No. 2.9e-08;

Matches 51; Conservative 30; Mismatches 93; Indels 36; Gaps 8;

QY 79 DIEGVVDYFTHIRNONGEMFGAGLPCGQVPEHEHMRWMTTEKKHAENFEFFCQL 138

DB 9 DTRALVAVFVGKYLKROKGVCGAGCEGPADPLHQAARAGDEFEFRRTFSDLAQL 68

QY 139 LAVP-----RISFSLYODVVRVGNADTDCPMYSGRLIGLSFGFVAAKMM--ES 188

DB 69 HTYPSAQOQRTQVSDLEFG-----GPNMGRVLAFLFCAALCAESVKNEM 115

QY 189 VELQGOVRNLFFVYTSLEFTRIRNMKEHNSWDEFTLQGMKBDYERAEAEKVGRRKQ 248

DB 116 EPLVGVQDEMNV---AYLETRL-VDMIHSSGMAEFETAL-----YCDGALAE-ARRLR 163

QY 249 NRKSMIGAGYTAGAIGIVGVCGRMFS 278

DB 164 EGNMASVRT-VLTGAVALGALVTGAFEPAS 192

## RESULT 12

AAW97392  
 ID AAW97392 standard; Protein; 193 AA.

AC AAW97392;

DT 20-MAY-1999 (first entry)

DE The human bcl-y protein.

KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;  
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
 KW head trauma; Alzheimer's disease; neural; muscular degenerative disease;  
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;  
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
 KW premature cell death; cell death stimulator; prolonged cell life span;  
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;  
 KW parasite.

XX Homo sapiens.

PN US5883229-A.

PD 16-MAR-1999.

PE 25-NOV-1997; 97US-0978523.

PR 23-FEB-1996; 96US-0012201.

PR 11-FEB-1997; 97US-0798897.

PR 25-NOV-1997; 97US-0978523.

PA (COCE-) COCENSYS INC.

PI Guastella J;

DR WPI: 1999-214150/18.

DR N-PSDB: AAX15946.

PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful  
 for modulating programmed cell death

PS Claim 1; Columns 17-18; 26pp; English.

XX The present sequence represents human bcl-y protein (Hbcl-y). The  
 CC specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and  
 CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in  
 CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y  
 CC proteins may be used to treat conditions associated with a disruption of  
 CC the cell death pathway. If they act as cell death inhibitors, they may be  
 CC used in therapies to treat subjects suffering from: strokes, head trauma,  
 CC Alzheimer's disease, neural and muscular degenerative diseases  
 CC (especially multiple sclerosis), myocardial infarction, vitally induced  
 CC cell death, aging, spinal cord injuries and amyotrophic lateral  
 CC sclerosis- conditions where cells under go premature cell death as a  
 CC result of triggers which may or may not be apparent. They may also be  
 CC used in this way to develop cell lines which remain viable in culture for  
 CC an extended period. In contrast, if they act as cell death stimulators,  
 CC Rbcl-y and Hbcl-y may be used to treat conditions associated with  
 CC prolonged cell life span such as cancer (especially Kaposi's sarcoma and  
 CC lung cancer) and auto/hyperimmune diseases. They may also be used to  
 CC cause cell death in, and hence control, parasites.

XX Sequence 193 AA;

Query Match 10.0%; Score 148; DB 20; Length 193;

Best Local Similarity 24.3%; Pred. No. 2.9e-08;





1  
2  
3  
4

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 24, 2003, 11:53:04 ; Search time 14 Seconds  
(without alignments)  
588,458 Million cell updates/sec

Title: US-09-993-420a-3

Perfect score: 1479  
Sequence: 1 MTRCTADNSLTNPATRRRM.....ACATGIVGVYCGRMFSLK 280

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/prodata/1/iaa/5a\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/iaa/5b\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/iaa/5a\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/iaa/5b\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/iaa/backfileasl.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1479	100.0	280	1	US-08-471-058-19 Sequence 19, Appl
2	1479	100.0	280	3	US-08-471-057-19 Sequence 19, Appl
3	1479	100.0	280	4	US-09-234-186-3 Sequence 3, Appl
4	1479	100.0	280	4	US-09-233-527-3 Sequence 3, Appl
5	1479	100.0	280	5	PCT-US93-05651-3 Sequence 3, Appl
6	156	10.5	27	2	US-08-733-505A-49 Sequence 49, Appl
7	156	10.5	27	2	US-08-706-741B-84 Sequence 84, Appl
8	156	10.5	27	2	US-08-924-695A-84 Sequence 84, Appl
9	151	10.2	192	1	US-08-978-897-5 Sequence 5, Appl
10	151	10.2	192	2	US-08-978-897-5 Sequence 5, Appl
11	151	10.2	193	1	US-08-798-897-3 Sequence 3, Appl
12	151	10.2	193	2	US-08-978-897-3 Sequence 3, Appl
13	148	10.0	193	1	US-08-978-897-6 Sequence 6, Appl
14	148	10.0	193	2	US-08-978-897-6 Sequence 6, Appl
15	148	10.0	193	1	US-08-978-897-4 Sequence 4, Appl
16	148	10.0	193	2	US-08-978-897-4 Sequence 4, Appl
17	135.5	9.2	225	4	US-09-101-519-1 Sequence 1, Appl
18	135	9.1	233	1	US-08-333-565-59 Sequence 59, Appl
19	135	9.1	233	1	US-08-081-448-6 Sequence 6, Appl
20	135	9.1	233	1	US-08-607-269-24 Sequence 24, Appl
21	135	9.1	233	2	US-08-471-058-14 Sequence 14, Appl
22	135	9.1	233	2	US-08-661-479-59 Sequence 59, Appl
23	135	9.1	233	2	US-08-470-670A-7 Sequence 7, Appl
24	135	9.1	233	3	US-08-471-057-14 Sequence 14, Appl
25	135	9.1	233	3	US-08-481-739-2 Sequence 2, Appl
26	135	9.1	233	4	US-09-167-921-2 Sequence 2, Appl
27	135	9.1	233	4	US-09-323-743-2 Sequence 2, Appl

28	135	9.1	233	4	US-08-461-511A-7 Sequence 7, Appl
29	135	9.1	233	5	PCT-US94-07089-7 Sequence 7, Appl
30	135	9.1	233	5	PCT-US95-04600-24 Sequence 24, Appl
31	132	8.9	233	4	US-09-271-014A-6 Sequence 6, Appl
32	126	8.5	365	4	US-09-149-476-696 Sequence 17, Appl
33	120.5	8.1	232	2	US-08-408-095-17 Sequence 17, Appl
34	119.5	8.1	232	2	US-08-408-095-18 Sequence 18, Appl
35	118.5	8.0	236	1	US-08-607-269-22 Sequence 22, Appl
36	118.5	8.0	236	4	US-09-127-048-9 Sequence 9, Appl
37	118.5	8.0	236	5	PCT-US95-04600-22 Sequence 22, Appl
38	117	7.9	239	2	US-08-365-486A-17 Sequence 17, Appl
39	117	7.9	239	2	US-08-408-095-16 Sequence 16, Appl
40	117	7.9	239	4	US-08-880-342-17 Sequence 17, Appl
41	116	7.8	233	1	US-08-607-269-23 Sequence 23, Appl
42	116	7.8	233	5	PCT-US95-04600-23 Sequence 23, Appl
43	116	7.8	239	1	US-08-112-208C-10 Sequence 10, Appl
44	116	7.8	239	1	US-08-248-819A-10 Sequence 10, Appl
45	116	7.8	239	1	US-08-607-269-20 Sequence 20, Appl

## ALIGNMENTS

RESULT 1  
US-08-471-058-19  
; Sequence 19, Application US/08471058  
; Patent No. 5770443  
; GENERAL INFORMATION:  
; APPLICANT: Kiefer, Michael C.  
; TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING  
; PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/471,058  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/320,157  
; FILING DATE: 07-OCT-1994  
; APPLICATION NUMBER: 08/160,067  
; FILING DATE: 30-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: lehnhardt, Susan K  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 23647-20007.12  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-813-5600  
; TELEFAX: 415-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ. ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 280 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-471-058-19  
Query Match 100.0%; Score 1479; DB 1; Length 280;  
Best Local Similarity 100.0%; Pred. No. 1,8e-164;

Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADOLPSPSRQASTRRM 60  
 Db 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADOLPSPSRQASTRRM 60

QY 61 SIGESIDKINDMEPRLDIEGFVVDYFTHRIKONGMEMFGAPGLPCGVQPEHEMMRYMG 120  
 Db 61 SIGESIDKINDMEPRLDIEGFVVDYFTHRIKONGMEMFGAPGLPCGVQPEHEMMRYMG 120

QY 121 TIFEKKAENFEFTCEQLLAVPRISFSLYQDVYRTVGNAGTDCPMSYGRILGLISFGGF 180  
 Db 121 TIFEKKAENFEFTCEQLLAVPRISFSLYQDVYRTVGNAGTDCPMSYGRILGLISFGGF 180

QY 181 VAAKMMESVELOGVRLNFYVTSLEFKTRIRNNMKEHNRSDDEMTLGKQKEDYERAEA 240  
 Db 181 VAAKMMESVELOGVRLNFYVTSLEFKTRIRNNMKEHNRSDDEMTLGKQKEDYERAEA 240

QY 241 EKVGRKONRRMSMTAGVTAGATGIVGVVCGRMFSLK 280  
 Db 241 EKVGRKONRRMSMTAGVTAGATGIVGVVCGRMFSLK 280

## RESULT 2

US-08-471-057-19  
 ; Sequence 19, Application US/08471057  
 ; Patent No. 6015687  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIEFER, MICHAEL C.  
 ; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA  
 ; NUMBER OF SEQUENCES: 22  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESS: MORRISON & FOERSTER  
 ; STREET: 755 Page Mill Road  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94304-1018  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/471,057  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/320,157  
 ; FILING DATE: 07-OCT-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: LEHNHARDT, SUSAN K.  
 ; REGISTRATION NUMBER: 33,943  
 ; REFERENCE/DOCKET NUMBER: 23647-20007.20  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 813-5600  
 ; TELEFAX: (415) 494-0792  
 ; TELEX: 706141  
 ; INFORMATION FOR SEQ. ID NO: 19:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 280 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-471-057-19

Query Match 100.0%; Score 1479; DB 3; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-164;  
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADOLPSPSRQASTRRM 60

Db 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADOLPSPSRQASTRRM 60  
 QY 61 SIGESIDKINDMEPRLDIEGFVVDYFTHRIKONGMEMFGAPGLPCGVQPEHEMMRYMG 120  
 Db 61 SIGESIDKINDMEPRLDIEGFVVDYFTHRIKONGMEMFGAPGLPCGVQPEHEMMRYMG 120

QY 121 TIFEKKAENFEFTCEQLLAVPRISFSLYQDVYRTVGNAGTDCPMSYGRILGLISFGGF 180  
 Db 121 TIFEKKAENFEFTCEQLLAVPRISFSLYQDVYRTVGNAGTDCPMSYGRILGLISFGGF 180

QY 181 VAAKMMESVELOGVRLNFYVTSLEFKTRIRNNMKEHNRSDDEMTLGKQKEDYERAEA 240  
 Db 181 VAAKMMESVELOGVRLNFYVTSLEFKTRIRNNMKEHNRSDDEMTLGKQKEDYERAEA 240

QY 241 EKVGRKONRRMSMTAGVTAGATGIVGVVCGRMFSLK 280  
 Db 241 EKVGRKONRRMSMTAGVTAGATGIVGVVCGRMFSLK 280

## RESULT 3

US-09-234-186-3  
 ; Sequence 3, Application US/09234186  
 ; Patent No. 6312947  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Horvitz, H. Robert  
 ; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A  
 ; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND  
 ; FILE REFERENCE: 01997/201005  
 ; CURRENT APPLICATION NUMBER: US/09/234,186  
 ; EARLIER FILING DATE: 1999-01-20  
 ; EARLIER APPLICATION NUMBER: 07/898,933  
 ; EARLIER FILING DATE: 1992-06-12  
 ; EARLIER APPLICATION NUMBER: 07/927,681  
 ; EARLIER FILING DATE: 1992-08-10  
 ; EARLIER APPLICATION NUMBER: 08/288,295  
 ; EARLIER FILING DATE: 1994-08-10  
 ; EARLIER APPLICATION NUMBER: 08/801,248  
 ; EARLIER FILING DATE: 1997-02-19  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 280  
 ; TYPE: PRT  
 ; ORGANISM: Caenorhabditis elegans  
 ; US-09-234-186-3

Query Match 100.0%; Score 1479; DB 4; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-164;  
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADOLPSPSRQASTRRM 60  
 Db 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADOLPSPSRQASTRRM 60

QY 61 SIGESIDKINDMEPRLDIEGFVVDYFTHRIKONGMEMFGAPGLPCGVQPEHEMMRYMG 120  
 Db 61 SIGESIDKINDMEPRLDIEGFVVDYFTHRIKONGMEMFGAPGLPCGVQPEHEMMRYMG 120

QY 121 TIFEKKAENFEFTCEQLLAVPRISFSLYQDVYRTVGNAGTDCPMSYGRILGLISFGGF 180  
 Db 121 TIFEKKAENFEFTCEQLLAVPRISFSLYQDVYRTVGNAGTDCPMSYGRILGLISFGGF 180

QY 181 VAAKMMESVELOGVRLNFYVTSLEFKTRIRNNMKEHNRSDDEMTLGKQKEDYERAEA 240  
 Db 181 VAAKMMESVELOGVRLNFYVTSLEFKTRIRNNMKEHNRSDDEMTLGKQKEDYERAEA 240

QY 241 EKVGRKONRRMSMTAGVTAGATGIVGVVCGRMFSLK 280  
 Db 241 EKVGRKONRRMSMTAGVTAGATGIVGVVCGRMFSLK 280



## RESULT 4

```

US-09-233-527-3
; Sequence 3, Application US/09233527
; Patent No. 645617
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hengartner, Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; TITLE OF INVENTION: USES THEREFOR
; FILE REFERENCE: 01997/201004
; CURRENT APPLICATION NUMBER: US/09/233,527
; CURRENT FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 07/898,933
; PRIOR FILING DATE: 1992-06-12
; PRIOR APPLICATION NUMBER: 07/927,681
; PRIOR FILING DATE: 1992-08-10
; PRIOR APPLICATION NUMBER: 08/288,295
; PRIOR FILING DATE: 1994-08-10
; PRIOR APPLICATION NUMBER: 08/801,248
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-233-527-3

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## Query Match

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Best Local Similarity 100.0%; Score 1479; DB 4; Length 280;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADOLPSPRSQASTRRM 60
DB 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADOLPSPRSQASTRRM 60
QY 61 SIGESIDKINDWERPRIDIEGFVVDYFTHIRONGMEMFGAPGLPCGVQPEHEMMRYMG 120
DB 61 SIGESIDKINDWERPRIDIEGFVVDYFTHIRONGMEMFGAPGLPCGVQPEHEMMRYMG 120
QY 121 TFEKKHAENFETFCOEQLAVPRISFLYQDVRTVGNADQDCPMYGRILGLISFGCF 180
DB 121 TFEKKHAENFETFCOEQLAVPRISFLYQDVRTVGNADQDCPMYGRILGLISFGCF 180
QY 181 VAKKMESEVLOGOVNLFVYTSLEFKTRIRNNKEHNRSMDDEFTLGKOKKEDYERAE 240
DB 181 VAKKMESEVLOGOVNLFVYTSLEFKTRIRNNKEHNRSMDDEFTLGKOKKEDYERAE 240
QY 241 EKVGRKORRRSMIGAGVTAGATGIVGVVCGRMFSLK 280
DB 241 EKVGRKORRRSMIGAGVTAGATGIVGVVCGRMFSLK 280

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## RESULT 5

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PCT-US93-05651-3
; Sequence 3, Application PC/TUS9305651
; GENERAL INFORMATION:
; TITLE OF INVENTION: A Gene Which Prevents Programmed Cell Death
; NUMBER OF SEQUENCES: 5
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05651
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-05651-3

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Query Match 100.0%; Score 1479; DB 5; Length 280;
Best Local Similarity 100.0%; Pred. No. 1.8e-164;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADOLPSPRSQASTRRM 60
DB 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADOLPSPRSQASTRRM 60
QY 61 SIGESIDKINDWERPRIDIEGFVVDYFTHIRONGMEMFGAPGLPCGVQPEHEMMRYMG 120
DB 61 SIGESIDKINDWERPRIDIEGFVVDYFTHIRONGMEMFGAPGLPCGVQPEHEMMRYMG 120
QY 121 TFEKKHAENFETFCOEQLAVPRISFLYQDVRTVGNADQDCPMYGRILGLISFGCF 180
DB 121 TFEKKHAENFETFCOEQLAVPRISFLYQDVRTVGNADQDCPMYGRILGLISFGCF 180
QY 181 VAKKMESEVLOGOVNLFVYTSLEFKTRIRNNKEHNRSMDDEFTLGKOKKEDYERAE 240
DB 181 VAKKMESEVLOGOVNLFVYTSLEFKTRIRNNKEHNRSMDDEFTLGKOKKEDYERAE 240
QY 241 EKVGRKORRRSMIGAGVTAGATGIVGVVCGRMFSLK 280
DB 241 EKVGRKORRRSMIGAGVTAGATGIVGVVCGRMFSLK 280

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## RESULT 6

```

US-08-733-505A-49
; Sequence 49, Application US/08733505A
; Patent No. 5856445

```

```

; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-733-505A-49

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## Query Match

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Best Local Similarity 100.0%; Score 156; DB 2; Length 27;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 73 WEPRLDIEGFVVDYFTHIRONGMEW 99
DB 1 WEPRLDIEGFVVDYFTHIRONGMEW 27

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RESULT 7  
US-08-706-741B-84  
Sequence 84, Application US/08706741B  
Patent No. 5935593  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, STANLEY J.  
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BLVD., SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: USA  
ZIP: 63146  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/706,741B  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 965017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 84:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-706-741B-84

Query Match 10.5%; Score 156; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.9e-11;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 73 WEPRLDIEGFVVDYFTHIRONGMEW 99  
|||||  
DB 1 WEPRLDIEGFVVDYFTHIRONGMEW 27

RESULT 8  
US-08-924-695A-84  
Sequence 84, Application US/08924695A  
Patent No. 5998583  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, STANLEY J.  
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BLVD., SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: USA  
ZIP: 63105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/924,695A

FILING DATE: 09-SEP-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 971798  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 84:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-924-695A-84

Query Match 10.5%; Score 156; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.9e-11;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 73 WEPRLDIEGFVVDYFTHIRONGMEW 99  
|||||  
DB 1 WEPRLDIEGFVVDYFTHIRONGMEW 27

RESULT 9  
US-08-798-897-5  
Sequence 5, Application US/08798897  
Patent No. 5789201  
GENERAL INFORMATION:  
APPLICANT: Gastella, John  
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/798,897  
FILING DATE: February 11, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1483.0140001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 192 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-798-897-5

Query Match 10.2%; Score 151; DB 1; Length 192;  
Best Local Similarity 24.3%; Pred. No. 1.7e-09;  
Matches 51; Conservative 31; Mismatches 92; Indels 36; Gaps 8;

OY 79 DICEFVVDYFTHIRONGMEFGAPGLFCGVPDEHMMRVKGIIFKHAENFETFCOL 138

Db 8 DTRALVADFGYKLRQGYVCGAGPEGCPADPLHQAAMRAAGDEFTFRRTFSDLAOL 67  
 QY 139 LAMP-----RISFSLYODVVRTVGNMOTDCCPMYSYGRLLIGLISFGFVAAKMM--ES 188  
 Db 68 HVTFGSAQQRFTQVSDLEFG-----GPNMGRVAFVFGAALCAESVAKEM 114  
 QY 189 VELQGVNLFVYTSLEFKTRIRNNMKEHNSMDPEMTLGKOMKEDYERAEKVRGRKQ 248  
 Db 115 EPLVGQVODMWV---TYLETRLA-DWIHSSGMAEFTAL-----YGDGALBE-ARRLR 162  
 QY 249 NRWSMIGAGVTAGAGIVGVVCGRMMS 278  
 Db 163 EGNMASVRT-VLTGAVALGALVTVGAFPAS 191

RESULT 10  
 US-08-978-523-5  
 ; Sequence 5, Application US/08978523  
 ; Patent No. 5883229  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Guastella, John  
 ; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2  
 ; TITLE OF INVENTION: Homologue  
 ; NUMBER OF SEQUENCES: 53  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 ; STREET: 1100 New York Avenue, N.W., Suite 600  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/978, 523  
 ; FILING DATE: herewith  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/798, 897  
 ; FILING DATE: February 11, 1997  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Esmond, Robert W.  
 ; REGISTRATION NUMBER: 32,893  
 ; REFERENCE/DOCKET NUMBER: 1483, 0140002  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-371-2540  
 ; TELEFAX: 202-371-2540  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 192 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: not relevant  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-978-523-5

Query Match 10.2%; Score 151; DB 2; Length 192;  
 Best Local Similarity 24.3%; Pred. No. 1.7e-09;  
 Matches 51; Conservative 31; Mismatches 92; Indels 36; Gaps 8;

QY 79 DIEGFVVDYFTHIRIRONGMEWFGAPGLPCGVOPHEHMMRWMTTFEKKHAENFTFCEOL 138  
 Db 8 DTRALVADFGYKLRQGYVCGAGPEGCPADPLHQAAMRAAGDEFTFRRTFSDLAOL 67  
 QY 139 LAMP-----RISFSLYODVVRTVGNMOTDCCPMYSYGRLLIGLISFGFVAAKMM--ES 188  
 Db 68 HVTFGSAQQRFTQVSDLEFG-----GPNMGRVAFVFGAALCAESVAKEM 114

QY 169 VELQGVNLFVYTSLEFKTRIRNNMKEHNSMDPEMTLGKOMKEDYERAEKVRGRKQ 248  
 Db 115 EPLVGQVODMWV---TYLETRLA-DWIHSSGMAEFTAL-----YGDGALBE-ARRLR 162  
 QY 249 NRWSMIGAGVTAGAGIVGVVCGRMMS 278  
 Db 163 EGNMASVRT-VLTGAVALGALVTVGAFPAS 191

RESULT 11  
 US-08-798-897-3  
 ; Sequence 3, Application US/08798897  
 ; Patent No. 5789201  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Guastella, John  
 ; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2  
 ; TITLE OF INVENTION: Homologue  
 ; NUMBER OF SEQUENCES: 53  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 ; STREET: 1100 New York Avenue, N.W., Suite 600  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/798, 897  
 ; FILING DATE: February 11, 1997  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Esmond, Robert W.  
 ; REGISTRATION NUMBER: 32,893  
 ; REFERENCE/DOCKET NUMBER: 1483, 0140001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-371-2600  
 ; TELEFAX: 202-371-2540  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 193 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: not relevant  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-798-897-3

Query Match 10.2%; Score 151; DB 1; Length 193;  
 Best Local Similarity 24.3%; Pred. No. 1.7e-09;  
 Matches 51; Conservative 31; Mismatches 92; Indels 36; Gaps 8;

QY 79 DIEGFVVDYFTHIRIRONGMEWFGAPGLPCGVOPHEHMMRWMTTFEKKHAENFTFCEOL 138  
 Db 9 DTRALVADFGYKLRQGYVCGAGPEGCPADPLHQAAMRAAGDEFTFRRTFSDLAOL 68  
 QY 139 LAMP-----RISFSLYODVVRTVGNMOTDCCPMYSYGRLLIGLISFGFVAAKMM--ES 188  
 Db 69 HVTFGSAQQRFTQVSDLEFG-----GPNMGRVAFVFGAALCAESVAKEM 115  
 QY 189 VELQGVNLFVYTSLEFKTRIRNNMKEHNSMDPEMTLGKOMKEDYERAEKVRGRKQ 248  
 Db 116 EPLVGQVODMWV---TYLETRLA-DWIHSSGMAEFTAL-----YGDGALBE-ARRLR 163  
 QY 249 NRWSMIGAGVTAGAGIVGVVCGRMMS 278  
 Db 164 EGNMASVRT-VLTGAVALGALVTVGAFPAS 192

RESULT 12  
 US-08-978-523-3

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? CORRESPONDENCE ADDRESS:
? ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
? STREET: 1100 New York Avenue, N.W., Suite 600
? CITY: Washington
? STATE: DC
? COUNTRY: USA
? ZIP: 20005
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/798, 897
? FILING DATE: February 11, 1997
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Rsmund, Robert W.
? REGISTRATION NUMBER: 32,893
? REFERENCE/DOCKET NUMBER: 1483.0140001
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202-371-2600
? TELEFAX: 202-371-2540
? INFORMATION FOR SEQ ID NO: 6:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 192 amino acids
? TYPE: amino acid
? STRANDEDNESS: not relevant
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-798-897-6

Query Match 10.0%; Score 148; DB 1; Length 192;
Best Local Similarity 24.3%; Pred. No. 3.8e-09;
Matches 51; Conservative 30; Mismatches 93; Indels 36; Gaps 8;

QY 79 DIEGVVYVFTHRIQNQNMENFGAGLFCGVQPEHMRKRWGCTIEFKKHAENFEFFCQL 138
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 8 DTRALVEFVGKLEKQKYVCGAGGEGSPADPLHQMRKAGDEFEFRFRFFSDLAQL 67

QY 139 LAVP-----RISFSIQDVVFRTVCNAQTDCPMYSYGRLLIGLISFCGFVAKKM--ES 188
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 68 HTVPESAQQRFTQVSDLEFG-----GPNMGRIVAFVFFAALCAESVKNEM 114

QY 189 VELQGVNLFVYVSLFTKTRIRNNKKEHNSWDEFTLIGQMKEDYERARAEKVGRRKQ 248
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 115 EPLVGQVQENVV--AYLETRLA-DWHSISGMAEFTEL-----YGDALAE-ARRLR 162

QY 249 NRRWSMIGAGVTAGIGIVGVCGRMFSS 278
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Db 163 EGNMAYVRT-VLTGAVALGALVTVGAFPPAS 191

RESULT 14
US-08-978-523-6
; Sequence 6, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-978-523-6

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Query Match 10.0%; Score 148; DB 2; Length 192;

Best Local Similarity 24.3%; Pred. No. 3.8e-09; Matches 51; Conservative 30; Mismatches 93; Indels 36; Gaps 8;

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QY 79 DIEGFVVDYFTHIRIRONGMFMGAPGLPCGVOPHEHMRVMTIFPKKHAENFETCEOL 138
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Db 8 DTRALVEDEVGYKLRQKGYCGAGPGEPADPLHQAMRAAGDEFETFRRTFSDLAOL 67
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QY 139 LAVP-----RISFSLYQDVVTVGNAGTDDCPMSYGRLLIGLISFGVPAAKMM--ES 188
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QY 189 VELGGVRLNFVYTSLEFKTRIRNNMKEHNRSMDDFMTLGKOMKEDYERAERKVRKQ 248
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QY 249 NRRMSMIGAGVTAGATIGVGVVCGRMFS 278
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Db 163 EGNMASVRT-VLTGAVALGALVTGAFAS 191
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RESULT 15  
US-08-798-897-4  
Sequence 4, Application US/08798897  
Patent No. 5789201

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; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; City: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.

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; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-798-897-4

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Query Match 10.0%; Score 148; DB 1; Length 193;

Best Local Similarity 24.3%; Pred. No. 3.8e-09; Matches 51; Conservative 30; Mismatches 93; Indels 36; Gaps 8;

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QY 79 DIEGFVVDYFTHIRIRONGMFMGAPGLPCGVOPHEHMRVMTIFPKKHAENFETCEOL 138
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 9 DTRALVEDEVGYKLRQKGYCGAGPGEPADPLHQAMRAAGDEFETFRRTFSDLAOL 68
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 139 LAVP-----RISFSLYQDVVTVGNAGTDDCPMSYGRLLIGLISFGVPAAKMM--ES 188
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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QY 189 VELGGVRLNFVYTSLEFKTRIRNNMKEHNRSMDDFMTLGKOMKEDYERAERKVRKQ 248
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 116 EPLVGQVQEMWV---AYLETRLA-DWIHSSGMAEFTAL-----YDGALEE-ARRLR 163
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 249 NRRMSMIGAGVTAGATIGVGVVCGRMFS 278
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 164 EGNMASVRT-VLTGAVALGALVTGAFAS 192
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Search completed: February 24, 2003, 11:55:26  
Job time : 15 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 24, 2003, 11:54:44 ; Search time 13 Seconds  
(Without alignments)  
669.196 Million cell updates/sec

Title: US-09-993-420a-3

Perfect score: 1479  
Sequence: 1 MTRCTADNSLTNPAYRRRTM.....AGALIGVGVVCGRMFSLK 280

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/1/pubppaa/PCCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubppaa/US07\_NEW\_PUB.pep:\*
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- 12: /cgn2\_6/ptodata/1/pubppaa/US10\_PUBCOMB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1479	100.0	280	US-10-101-482-19	Sequence 19, Appl
2	154	10.4	193	US-09-925-674A-9	Sequence 9, Appl
3	150	10.1	193	US-09-925-674A-7	Sequence 7, Appl
4	135	9.1	233	US-10-101-482-14	Sequence 14, Appl
5	135	9.1	233	US-09-734-846-2	Sequence 2, Appl
6	135	9.1	233	US-09-952-278-6	Sequence 6, Appl
7	132	8.9	152	US-10-158-769-2	Sequence 1, Appl
8	122.5	8.3	155	US-10-158-769-1	Sequence 12, Appl
9	116	7.8	239	US-10-101-482-12	Sequence 5, Appl
10	114	7.7	239	US-08-726-211-5	Sequence 40954, A
11	99	6.7	185	US-09-864-761-40954	Sequence 2, Appl
12	96	6.5	235	US-10-208-155-2	Sequence 15, Appl
13	95	6.4	226	US-10-101-482-15	Sequence 7, Appl
14	90.5	6.1	205	US-08-726-211-7	Sequence 4, Appl
15	90.5	6.1	204	US-09-952-278-4	Sequence 306, App
16	90	6.1	275	US-09-741-669-106	Sequence 2, Appl
17	89	6.0	190	US-09-952-278-2	Sequence 55, Appl
18	83	5.6	444	US-09-464-099A-55	Sequence 55, Appl
19	83	5.6	444	US-09-861-696-55	Sequence 55, Appl

20	82.5	5.6	447	US-09-843-250-23	Sequence 23, Appl
21	82	5.5	1814	US-09-920-552-103	Sequence 103, App
22	82	5.5	4342	US-09-815-242-5107	Sequence 5107, Ap
23	81.5	5.5	444	US-09-464-099A-53	Sequence 53, Appl
24	81.5	5.5	444	US-09-861-696-53	Sequence 53, Appl
25	80.5	5.4	471	US-09-765-272-158	Sequence 158, App
26	80	5.4	539	US-09-935-145-6	Sequence 6, Appl
27	80	5.4	558	US-09-925-301-1329	Sequence 1329, Ap
28	80	5.4	623	US-09-862-007-4	Sequence 4, Appl
29	80	5.4	1332	US-09-982-091A-4	Sequence 4, Appl
30	79.5	5.4	372	US-09-815-242-11156	Sequence 11156, A
31	79.5	5.4	649	US-09-815-242-13206	Sequence 13206, A
32	79.5	5.4	650	US-09-815-242-13206	Sequence 13667, A
33	78.5	5.4	1701	US-09-963-959-2	Sequence 2, Appl
34	78.5	5.3	444	US-09-464-099A-54	Sequence 54, Appl
35	78.5	5.3	444	US-09-861-696-54	Sequence 54, Appl
36	78.5	5.3	543	US-09-738-626-5237	Sequence 5237, Ap
37	78	5.3	172	US-10-101-482-16	Sequence 16, Appl
38	78	5.3	441	US-09-970-711-26	Sequence 26, Appl
39	78	5.3	445	US-10-076-622-473	Sequence 473, App
40	78	5.3	445	US-09-825-301-29	Sequence 29, Appl
41	78	5.3	445	US-09-604-287A-473	Sequence 473, App
42	78	5.3	445	US-10-007-805-473	Sequence 473, App
43	78	5.3	449	US-09-843-250-20	Sequence 20, Appl
44	78	5.3	1341	US-10-076-622-565	Sequence 565, App
45	78	5.3	1341	US-10-007-805-565	Sequence 565, App

#### ALIGNMENTS

RESULT 1  
US-10-101-482-19  
; Sequence 19, Application US/10101482  
; Publication NO. US2003000837A1  
; GENERAL INFORMATION:  
; APPLICANT: KIEFER, MICHAEL C.  
; BARR, PHILIP J.  
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA  
; ENCODING THE PROTEINS AND METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; City: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/101,482  
; FILING DATE: 18-Mar-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/320,157  
; FILING DATE: 07-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LEHNHARDT, SUSAN K.  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 23647-20007.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEFAX: 706141  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 280 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single

TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-10-101-482-19

Query Match 100.0%; Score 1479; DB 9; Length 280;  
Best Local Similarity 100.0%; Pred. No. 3.8e-149;  
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRCTADNSLTPAYRRRTMATGEMKEFLIGKTEPTDFGINSADOLDPSRQASTRRM 60  
DB 1 MTRCTADNSLTPAYRRRTMATGEMKEFLIGKTEPTDFGINSADOLDPSRQASTRRM 60  
QY 61 SIGESIDGKINDMEEPRLDEGVDFTHIRONGMEMFGAGLPCGVQPEHEMRVNG 120  
DB 61 SIGESIDGKINDMEEPRLDEGVDFTHIRONGMEMFGAGLPCGVQPEHEMRVNG 120  
QY 121 TIEFKHAENFETFECDLLAVPRISLSYQDVVRYGNAQTDQCPMSYGRLLISFGGF 180  
DB 121 TIEFKHAENFETFECDLLAVPRISLSYQDVVRYGNAQTDQCPMSYGRLLISFGGF 180  
QY 181 VAAKMSVELQOVRLFYTSLFKTRIRNNWKEHNSWDPFILGKOMKEDYERAA 240  
DB 181 VAAKMSVELQOVRLFYTSLFKTRIRNNWKEHNSWDPFILGKOMKEDYERAA 240  
QY 241 EKVGRKONRRMSMIGAGYTAGAIGIVGVCGRMFSLK 280  
DB 241 EKVGRKONRRMSMIGAGYTAGAIGIVGVCGRMFSLK 280

RESULT 2  
US-09-925-674A-9  
; Sequence 9, Application US/09925674A  
; Patent No. US20020119943A1  
; GENERAL INFORMATION:  
; APPLICANT: AMRAD Operations Pty Ltd  
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2  
; FILE REFERENCE: 11686a  
; CURRENT APPLICATION NUMBER: US/09/925,674A  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/925,674  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: PN8965  
; PRIOR FILING DATE: 1996-03-27  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 193  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-925-674A-9

Query Match 10.4%; Score 154; DB 10; Length 193;  
Best Local Similarity 24.8%; Pred. No. 9.9e-09;  
Matches 52; Conservative 30; Mismatches 92; Indels 36; Gaps 8;

QY 79 DIEGFVVDYFTHIRONGMEMFGAGLPCGVQPEHEMRVNGTIEFKHAENFETFECDL 138  
DB 9 DTRALVADYFVYTKRKGKGYCGAGPBGADPLHQAARAGDEFTFRRTFSDLAQL 68  
QY 139 LAVP-----RISFSLYQDVVRYGNAQTDQCPMSYGRLLISFGGFAAKMM--ES 188  
DB 69 HVTGSAOQRFYOVDELFG-----GPNMGRVAFVFGALCAESVKNEM 115  
QY 189 VELQOVRLFYTSLFKTRIRNNWKEHNSWDPFILGKOMKEDYERAAEKVGRKQ 248  
DB 116 EPLVGQVDMVY---AYLETRLA-DWISSGGMAEFYAL-----YDGALEE-ARRLR 163  
QY 249 NRRMSMIGAGYTAGAIGIVGVCGRMFSLK 278  
DB 164 EGNMASVRT-VLTGAVVALGALVTYGAFFAS 192

RESULT 3  
US-09-925-674A-7  
; Sequence 7, Application US/09925674A  
; Patent No. US20020119943A1  
; GENERAL INFORMATION:  
; APPLICANT: AMRAD Operations Pty Ltd  
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2  
; FILE REFERENCE: 11686a  
; CURRENT APPLICATION NUMBER: US/09/925,674A  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/925,674  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: PN8965  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 193  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-09-925-674A-7

Query Match 10.1%; Score 150; DB 10; Length 193;  
Best Local Similarity 24.3%; Pred. No. 2.0e-08;  
Matches 51; Conservative 30; Mismatches 93; Indels 36; Gaps 8;

QY 79 DIEGFVVDYFTHIRONGMEMFGAGLPCGVQPEHEMRVNGTIEFKHAENFETFECDL 138  
DB 9 DTRALVADYFVYTKRKGKGYCGAGPBGADPLHQAARAGDEFTFRRTFSDLAQL 68  
QY 139 LAVP-----RISFSLYQDVVRYGNAQTDQCPMSYGRLLISFGGFAAKMM--ES 188  
DB 69 HVTGSAOQRFYOVDELFG-----GPNMGRVAFVFGALCAESVKNEM 115  
QY 189 VELQOVRLFYTSLFKTRIRNNWKEHNSWDPFILGKOMKEDYERAAEKVGRKQ 248  
DB 116 EPLVGQVDMVY---AYLETRLA-DWISSGGMAEFYAL-----YDGALEE-ARRLR 163  
QY 249 NRRMSMIGAGYTAGAIGIVGVCGRMFSLK 278  
DB 164 EGNMASVRT-VLTGAVVALGALVTYGAFFAS 192

RESULT 4  
US-10-101-482-14  
; Sequence 14, Application US/10101482  
; Publication No. US20030008837A1  
; GENERAL INFORMATION:  
; APPLICANT: KIEFER, MICHAEL C.  
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA  
; ENCODING THE PROTEINS AND METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/101,482  
; FILING DATE: 18-Mar-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/320,157  
; FILING DATE: 07-Oct-1994



ATTORNEY/AGENT INFORMATION:  
NAME: LEHNHARDT, SUSAN K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 23647-20007.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 233 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-10-101-482-14

Query Match  
Best Local Similarity 21.3%; Score 135; DB 9; Length 233;  
Matches 53; Conservative 38; Mismatches 82; Indels 76; Gaps 10;

QY 84 VVDYFTHIRIRONGMEWF-----GAPGLPCGVQPEHE----- 114  
||| : : : : :  
DB 9 VVDLSYKLSQKGYSGWSQSDVEENRTAEPECTESEMETPSAINGNPSMHLADSPAVNGA 68  
QY 115 -----MMRVNGTIFEKKHAENFETCEQLLAVPRISFLYQDYVR 154  
DB 69 TGHSSSLDAREVYIPMAAVKQALREAGDEFELRYRAFSDLTSQHLHTPGTAYOSFEQVYN 128  
QY 155 TVGNAQOTDCCPSYGRLLIGLISFGGFVAAKMESV--ELQGVNRLFVYTSLFTKIRN 212  
DB 129 -----ELFRDGVNMGRIYAFESFGG---ALCVESVDKEMQVLVSRIAMMATYLDHL-E 179  
QY 213 NMKEHNSWDDFMTLQKQKEDY-ERRAEKVGRRKONRMSMIGAGVTAGATIGVYV 271  
DB 180 PMIQENGMDTVEL-----YGNNAAESRKQGERFRNFWLTG-----MTVAGVVL 225  
QY 272 CGRMFSLK 280  
DB 226 LG-SLFSRK 233

RESULT 5  
US-09-734-846-2  
Sequence 2, Application US/09734846  
Patent No. US20010007025A1  
GENERAL INFORMATION:  
APPLICANT: Bennett, C. Frank  
APPLICANT: Dean, Nicholas M.  
APPLICANT: Monia, Brett P.  
APPLICANT: Nickoloff, Brian J.  
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
FILE REFERENCE: ISPH-0528  
CURRENT APPLICATION NUMBER: US/09/734, 846  
CURRENT FILING DATE: 2000-12-12  
PRIOR APPLICATION NUMBER: 09/277,020  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 09/167,921  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 09/323,743  
PRIOR FILING DATE: 1999-06-02  
NUMBER OF SEQ ID NOS: 74  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 233  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-734-846-2

Query Match  
Best Local Similarity 21.3%; Score 135; DB 10; Length 233;  
Matches 53; Conservative 38; Mismatches 82; Indels 76; Gaps 10;

QY 84 VVDYFTHIRIRONGMEWF-----GAPGLPCGVQPEHE----- 114  
||| : : : : :  
DB 9 VVDLSYKLSQKGYSGWSQSDVEENRTAEPECTESEMETPSAINGNPSMHLADSPAVNGA 68  
QY 115 -----MMRVNGTIFEKKHAENFETCEQLLAVPRISFLYQDYVR 154  
DB 69 TGHSSSLDAREVYIPMAAVKQALREAGDEFELRYRAFSDLTSQHLHTPGTAYOSFEQVYN 128  
QY 155 TVGNAQOTDCCPSYGRLLIGLISFGGFVAAKMESV--ELQGVNRLFVYTSLFTKIRN 212  
DB 129 -----ELFRDGVNMGRIYAFESFGG---ALCVESVDKEMQVLVSRIAMMATYLDHL-E 179  
QY 213 NMKEHNSWDDFMTLQKQKEDY-ERRAEKVGRRKONRMSMIGAGVTAGATIGVYV 271  
DB 180 PMIQENGMDTVEL-----YGNNAAESRKQGERFRNFWLTG-----MTVAGVVL 225  
QY 272 CGRMFSLK 280  
DB 226 LG-SLFSRK 233

RESULT 6  
US-09-952-278-6  
Sequence 6, Application US/09952278  
Patent No. US20020137182A1  
GENERAL INFORMATION:  
APPLICANT: Thompson, Craig B.  
APPLICANT: Bolise, Lawrence H.  
TITLE OF INVENTION: Vertebrate Apoptosis Gene:  
Compositions and Methods  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Arnold, White & Durkee  
STREET: 321 No. US20020137182A1th Clark Street, Suite 800  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60610  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/952,278  
FILING DATE: 12-Sep-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/081,448  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: NO. US20020137182A1thrup, Thomas E.  
REGISTRATION NUMBER: 33,268  
REFERENCE/DOCKET NUMBER: ARCD090  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-744-0090  
TELEFAX: 312-755-4489  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 233 amino acids  
TYPE: amino acid  
MOLECULE TYPE: protein  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-952-278-6

Query Match  
Best Local Similarity 21.3%; Score 135; DB 10; Length 233;  
Matches 53; Conservative 38; Mismatches 82; Indels 76; Gaps 10;

QY 84 VVDYFTHIRIRONGMEWF-----GAPGLPCGVQPEHE----- 114  
||| : : : : :  
DB 9 VVDLSYKLSQKGYSGWSQSDVEENRTAEPECTESEMETPSAINGNPSMHLADSPAVNGA 68  
QY 115 -----MMRVNGTIFEKKHAENFETCEQLLAVPRISFLYQDYVR 154  
DB 69 TGHSSSLDAREVYIPMAAVKQALREAGDEFELRYRAFSDLTSQHLHTPGTAYOSFEQVYN 128  
QY 155 TVGNAQOTDCCPSYGRLLIGLISFGGFVAAKMESV--ELQGVNRLFVYTSLFTKIRN 212  
DB 129 -----ELFRDGVNMGRIYAFESFGG---ALCVESVDKEMQVLVSRIAMMATYLDHL-E 179  
QY 213 NMKEHNSWDDFMTLQKQKEDY-ERRAEKVGRRKONRMSMIGAGVTAGATIGVYV 271  
DB 180 PMIQENGMDTVEL-----YGNNAAESRKQGERFRNFWLTG-----MTVAGVVL 225  
QY 272 CGRMFSLK 280  
DB 226 LG-SLFSRK 233

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Db      9 VVDPLSYKLSOKGYSWQSOFSDVEENRTEAPECTESEMETPSAINGNPMSHLADSPAVNGA 68
QY      115 -----MMRVMTLFEKKHAENFETPCQQLAVPRISFSLYQDVYR 154
;      : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db      69 TAHSSSLDAREVYIPMAAKVQALREAGDEFELRRRAFSDDLSQLHTPTAYQSEQVYN 128
QY      155 TVGNACTOCQPMSTYRLIGLISFGFVAAKMMESV--ELQGVNRLFVYTSLEFKTRIRN 212
;      : : : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db      129 -----ELFRDGVNMGRIYAFVFFSG--ALCVESYDKEMQVLVSRIAMMATYLNDEL-E 179
QY      213 NMKEHNRSDDEMTLGKMKEDY--ERAEAEVGRKKRKNRSMIGAGVTAGATIGVYV 271
;      : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db      180 PMIQNGSGMDTFVEL-----YGNMAAESRKQGERNRWFLTG-----MTVAGVYL 225
QY      272 CGRMFSLK 280
;      : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db      226 LG-SLFSRK 233

RESULT 7
US-10-158-769-2
; Sequence 2, Application US/10158769
; Publication No. US20030008924A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Shaomeng
; TITLE OF INVENTION: Small Molecule Antagonists of BCL-2 Family Protein
; FILE REFERENCE: UM-07232
; CURRENT APPLICATION NUMBER: US/10/158,769
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/293,983
; PRIOR FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-158-769-2

Query Match      8.9%; Score 132; DB 9; Length 152;
Best Local Similarity 24.5%; Pred. No. 1.5e-06;
Matches 38; Conservative 31; Mismatches 66; Indels 20; Gaps 6;

QY      84 VVDYFTHIRIRONGMWF-----GAPGLPCGVQPE--HEMRVMTGTFEKKHAENFET 134
;      : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db      5 VVDPLSYKLSOKGYSWQSOFSDVEENRTEAPECTESEMETPSAINGNPMSHLADSPAVNGA 68
QY      135 CEQLLAVPRISFSLYQDVYRTVGNACTOCQPMSTYRLIGLISFGFVAAKMMESV--ELQ 192
;      : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db      65 TSQHLHTPTAYQSEQVYN-----ELFRDGVNMGRIYAFVFFSG--ALCVESYDKEMQ 116
QY      193 GOVNRLEFVYTSLEFKTRIRNMMKEHNRSDDEMTL 227
;      : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db      117 VVVSRIAMMATYLNDEL-EPWIQNGSGMDTFVEL 150

RESULT 8
US-10-158-769-1
; Sequence 1, Application US/10158769
; Publication No. US20030008924A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Shaomeng
; TITLE OF INVENTION: Small Molecule Antagonists of BCL-2 Family Protein
; FILE REFERENCE: UM-07232
; CURRENT APPLICATION NUMBER: US/10/158,769
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/293,983
; PRIOR FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 3

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-158-769-1

Query Match      8.3%; Score 122.5; DB 9; Length 155;
Best Local Similarity 22.8%; Pred. No. 1.6e-05;
Matches 36; Conservative 32; Mismatches 67; Indels 23; Gaps 5;

QY      84 VVDYFTHIRIRONGMWF-----AGLPCGVQPEHEMRVMTGTFEKKHAENF 131
;      : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db      5 VVYTHIRKLSQKGYEWDADVGAPGAAPGCISSQPVVHLTRQAGDDFSRRYRDF 64
QY      132 ETPCEQLLAVPRISFSLYQDVYRTVGNACTOCQPMSTYRLIGLISFGFVAAKMMESV-- 189
;      : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db      65 AEMSRQLHLPTFARGRAFVVE-----ELFRDGVNMGRIYAFVFFSGVVC--VESYNR 116
QY      190 ELQGVNRLFVYTSLEFKTRIRNMMKEHNRSDDEMTL 227
;      : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db      117 EMSPLVDNIALMWTETYLNRHL-HTWIQNGSGMDAFVEL 153

RESULT 9
US-10-101-482-12
; Sequence 12, Application US/10101482
; Publication No. US20030008837A1
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; ENCODING THE PROTEINS AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/101,482
; FILING DATE: 18-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-101-482-12

Query Match      7.8%; Score 116; DB 9; Length 239;

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Best Local Similarity 19.4%; Pred. No. 0.00015;  
Matches 48; Conservative 39; Mismatches 76; Indels 84; Gaps 10;

QY 79 DIEGFVVDYFTHIRONGMEWF----- 100  
| : : : : :  
Db 10 DNEIIVWKYIHYKLSQGYENDAGDVGAAPGAPAGCIFSOPGHTPHTAASRDVART 69  
QY 101 -----GAPGLPGC-----VOP-EHEMMRWGTIEKKHAENFEFCOLLAVPRISFL 148  
| : : : : :  
Db 70 SPLQTPAPGAAGPALSPVPVHLLRQAGDDFSRRYRDFAMSSROLHLTPPTARGR 129  
QY 149 YQDVYRTVGNAGTQDCPMSYGRLLGLISFGGFVAAKMMESV--ELQGVNRLFVYTSLEFI 206  
| : : : : :  
Db 130 FATVE-----ELFRDGVNMGRIVAFFEEFGVWC---VESYNREMSPLVDNALMTETYL 181  
QY 207 KTRIRNNKKEHNSWDDEFTL-GKQMKEDYERAEAEKVRKKQNRW-----SMIG 256  
| : : : : :  
Db 182 NRHL-HTWIODNGMDAFVELYGPSMRPLDPS-----WLSKTLTSLALVG 227

QY 257 AGVTAGA 263  
| : : : : :  
Db 228 ACITLGA 234

RESULT 10  
US-08-726-211-5  
; Sequence 5, Application US/08726211  
; Publication No. US20030012812A1  
; GENERAL INFORMATION:  
; APPLICANT: Torno, Mar  
; APPLICANT: Tarl, Ana M.  
; APPLICANT: Lopez-Berestein, Gabriel  
; TITLE OF INVENTION: INHIBITION OF Bcl-2 PROTEIN EXPRESSION BY  
; TITLE OF INVENTION: LIPOSOMAL ANTISENSE OLIGODEOXYNUCLEOTIDES  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/726,211  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wilson, Mark B.  
; REGISTRATION NUMBER: 37,259  
; REFERENCE/DOCKET NUMBER: UTXC:504  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 239 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-726-211-5

Query Match 7.7%; Score 114; DB 1; Length 239;  
Best Local Similarity 19.4%; Pred. No. 0.00024;  
Matches 48; Conservative 39; Mismatches 76; Indels 84; Gaps 10;

QY 79 DIEGFVVDYFTHIRONGMEWF----- 100  
| : : : : :  
Db 10 DNEIIVWKYIHYKLSQGYENDAGDVGAAPGAPAGCIFSOPGHTPHTAASRDVART 69

QY 101 -----GAPGLPGC-----VOP-EHEMMRWGTIEKKHAENFEFCOLLAVPRISFL 148  
| : : : : :  
Db 70 SPLQTPAPGAAGPALSPVPVHLLRQAGDDFSRRYRDFAMSSROLHLTPPTARGR 129  
QY 149 YQDVYRTVGNAGTQDCPMSYGRLLGLISFGGFVAAKMMESV--ELQGVNRLFVYTSLEFI 206  
| : : : : :  
Db 130 FATVE-----ELFRDGVNMGRIVAFFEEFGVWC---VESYNREMSPLVDNALMTETYL 181  
QY 207 KTRIRNNKKEHNSWDDEFTL-GKQMKEDYERAEAEKVRKKQNRW-----SMIG 256  
| : : : : :  
Db 182 NRHL-HTWIODNGMDAFVELYGPSMRPLDPS-----WLSKTLTSLALVG 227

QY 257 AGVTAGA 263  
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Db 228 ACITLGA 234

RESULT 11  
US-09-864-761-40954  
; Sequence 40954, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO  
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
; FILE REFERENCE: Aeomlca-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1  
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; LENGTH: 185  
; TYPE: PRT

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Query Match 6.48; Score 95; DB 9; Length 226;

Best Local Similarity 25.2%; Pred. No. 0.023;  
Matches 31; Conservative 26; Mismatches 36; Indels 30; Gaps 7;

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DB 95 GVOENHE-----TVFCGLMRKLDIKNE-----DVKSLSRMHVFSQGV----- 134  
QY 164 CPMSYGRLLGLISFGFVAAKMESEVLOGVBNLF-VYTSLEFKIRIRNNKHEHNSMD 222  
DB 135 --TNGMIVTLISFGAFV-AKHAKTINQESCIPLEASTIDLVKRT--KRDWLVKORQMD 189  
QY 223 DFM 225  
DB 190 GFV 192

## RESULT 14

US-08-726-211-7  
; Sequence 7, Application US/08726211  
; Publication No. US20030012612A1  
; GENERAL INFORMATION:  
; APPLICANT: Tormo, Mar  
; APPLICANT: Tari, Ana M.  
; TITLE OF INVENTION: INHIBITION OF Bcl-2 PROTEIN EXPRESSION BY  
; NUMBER OF INVENTIONS: LIPOSOMAL ANTISENSE OLIGODEOXYNUCLEOTIDES  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/726,211  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wilson, Mark B.  
; REGISTRATION NUMBER: 37,259  
; REFERENCE/DOCKET NUMBER: UTXC:504  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 205 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-726-211-7

Query Match 6.1%; Score 90.5; DB 1; Length 205;  
Best Local Similarity 19.0%; Pred. No. 0.06;

Matches 37; Conservative 30; Mismatches 67; Indels 61; Gaps 7;

QY 79 DIEGVYVDYFTHIRIRONGEMWF----- 100  
DB 10 DNREIVMKYIHYKLSQRYEMDAGVGAAPGAPARPGIFSSQPGHTPHPAASRDVPART 69  
QY 101 -----GAGGLPCG-----VQP-EHEMMRYMGTFIEKHAENFEFFCQDLAVPRISFL 148  
DB 70 SPLQTPAAPGAAGAPALSPVPVHLLRQAGDDFSRRYRGDFAMSSQLHLTPPTAAGR 129  
QY 149 YQDVYRVGNATQDCPMSYGRLLGLISFGFVAAKMESEV--ELQGVBNLFVYTSLEFI 206  
DB 130 FATVVE-----ELFRDGVNMGRIVAFPEFGVVC--VESVNRKMSPLVDNALMTETYL 181

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DB 182 NRHL-HTWIDNGW 195

## RESULT 15

US-09-952-278-4

; Sequence 4, Application US/09952278  
; Patent No. US20020137182A1  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Craig B.  
; APPLICANT: Boise, Lawrence H.

; TITLE OF INVENTION: Vertebrate Apoptosis Gene:  
; Compositions and Methods

; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: 321 No. US20020137182A1th Clark Street, Suite 800  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60610

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/952,278  
; FILING DATE: 12-Sep-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/081,448  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. US20020137182A1thrup, Thomas E.  
; REGISTRATION NUMBER: 33,268  
; REFERENCE/DOCKET NUMBER: ARCD090  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-744-0090  
; TELEFAX: 312-755-4489  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 205 amino acids  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-952-278-4

Query Match 6.1%; Score 90.5; DB 10; Length 205;  
Best Local Similarity 19.0%; Pred. No. 0.06;

Matches 37; Conservative 30; Mismatches 67; Indels 61; Gaps 7;

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DB 10 DNREIVMKYIHYKLSQRYEMDAGVGAAPGAPARPGIFSSQPGHTPHPAASRDVPART 69  
QY 101 -----GAGGLPCG-----VQP-EHEMMRYMGTFIEKHAENFEFFCQDLAVPRISFL 148  
DB 70 SPLQTPAAPGAAGAPALSPVPVHLLRQAGDDFSRRYRGDFAMSSQLHLTPPTAAGR 129  
QY 149 YQDVYRVGNATQDCPMSYGRLLGLISFGFVAAKMESEV--ELQGVBNLFVYTSLEFI 206  
DB 130 FATVVE-----ELFRDGVNMGRIVAFPEFGVVC--VESVNRKMSPLVDNALMTETYL 181  
QY 207 KTRIRNNKHEHNSW 221  
DB 182 NRHL-HTWIDNGW 195

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us-09-993-420a-3.rapb

Page 8

Search completed: February 24, 2003, 11:59:22  
Job time : 13 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

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(without alignments)  
1253.648 Million cell updates/sec

Title: US-09-993-420A-3

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Searched: 4569144 seqs, 644733110 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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8	1479	100.0	280	23	US-09-993-420A-3	Sequence 3, Appli
9	1479	100.0	280	25	US-10-101-482-19	Sequence 19, Appli
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23	1479	100.0	280	21	US-09-791-537-46654	Sequence 46654, A
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32	1479	100.0	280	24	PCT-US02-03547-18	Sequence 18, Appli
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#### ALIGNMENTS

Result 1  
; Sequence 3, Application US/07927/681  
; GENERAL INFORMATION:  
; APPLICANT: Horvitz, H. Robert  
; APPLICANT: Hengartner, Michael  
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A  
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02173-4799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/927,681  
; FILING DATE: 10-AUG-1992  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 32,227

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1  REFERENCE/DOCKET NUMBER:  MIT-5934A
2
3  TELECOMMUNICATION INFORMATION:
4
5  TELEPHONE:  (617) 861-6240
6
7  TELEFAX:  (617) 861-9540
8
9  TELEX:  951794
10
11 INFORMATION FOR SEQ ID NO: 3:
12
13 SEQUENCE CHARACTERISTICS:
14
15 LENGTH: 280 amino acids
16
17 TYPE: amino acid
18
19 TOPOLOGY: linear
20
21 MOLECULE TYPE: protein
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Query Match	100.0%;	Score 1479;	DB 3;	Length 280;
Best Local Similarity	100.0%;	Pred. No. 3.3e-152;		
Matches 280; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	MTROCAADSLNPNPYARRRTMATGSMKEFLGKGTPEPDFGINSAPDLSPSPROASTRRM	60
Db	1	MTROCAADSLNPNPYARRRTMATGSMKEFLGKGTPEPDFGINSAPDLSPSPROASTRRM	60
QY	61	SIGESIDKINDMEEPRLDIEGVVDYFTTHIRIONGMEMFGAPGLPCGVOPBEHMMRVG	120
Db	61	SIGESIDKINDMEEPRLDIEGVVDYFTTHIRIONGMEMFGAPGLPCGVOPBEHMMRVG	120
QY	121	TTFEKKHAENEFCEOLAVPRISFSLYQOVVATYVNAQDQCPMSYGRILIGLISRGF	180
Db	121	TTFEKKHAENEFCEOLAVPRISFSLYQOVVATYVNAQDQCPMSYGRILIGLISRGF	180
QY	181	VAAKMSEVESLOGOVRLNFVYTSLEIKTRIINNKKEHNRSWDEMTLGOKMEDYERAEA	240
Db	181	VAAKMSEVESLOGOVRLNFVYTSLEIKTRIINNKKEHNRSWDEMTLGOKMEDYERAEA	240
QY	241	EKVGRKRONRRMSMGAATVAGATGICVGVVYVCGHMFSLK	280
Db	241	EKVGRKRONRRMSMGAATVAGATGICVGVVYVCGHMFSLK	280

RESULT 2  
US-08-288-295-3  
Sequence 3, Application US/08288295  
GENERAL INFORMATION:  
APPLICANT: Horvitz, H. Robert  
APPLICANT: Hengartner, Michael  
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A  
TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED  
TITLE OF INVENTION: CELL DEATH AND USES THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & RICHARDSON  
STREET: 225 Franklin Street, Suite 3100  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A. (F) ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/288,295  
FILING DATE: 10-AUG-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/927,681  
FILING DATE: 10-AUG-1992  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 01997/201003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070

```

: TELEFAX: (617) 542-8906
:
: TELE: 200154
: INFORMATION FOR SEQ ID NO: 3
: SEQUENCE CHARACTERISTICS:
: LENGTH: 280 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
: US-08-286-295-3

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Query Match	100.0%;	Score 1479;	DB 6;	Length 280;
Best Local Similarity	100.0%;	Pred. No. 3.3e-152;		
Matches 280; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	MTROCTANSLNTPYRRRTATAGMKFELGKCEPDPFINDADLPSPSQASTRM	60
Dd	1	MTRCTADNSLTNPYRRRTATAGMKFELGKCEPDPFINDADLPSPSQASTRM	60
QY	61	SIGESIDOKINDMEEPRIIDIEGFVVDYFTHIRIONGEMWFAGLPQGVOPHEHMRVWG	120
Dd	61	SIGESIDOKINDMEEPRIIDIEGFVVDYFTHIRIONGEMWFAGLPQGVOPHEHMRVWG	120
QY	121	TIFEKKAHENETFECDLIANPRISFELXYDVAITYVNAOTDOPMSYGRILGISPGF	180
Dd	121	TIFEKKAHENETFECDLIANPRISFELXYDVAITYVNAOTDOPMSYGRILGISPGF	180
QY	181	VAAKMMSEVELOQGVRLNLFVYTSLFITRIIRNNMKEHNRSMDDFMTLGKOMKEDYEREA	240
Dd	181	VAAKMMSEVELOQGVRLNLFVYTSLFITRIIRNNMKEHNRSMDDFMTLGKOMKEDYEREA	240
QY	241	EKVGRKKONRRMSMIGAGVYTGALIGIYVYVCGMMMSLK	280
Dd	241	EKVGRKKONRRMSMIGAGVYTGALIGIYVYVCGMMMSLK	280

RESULT 3  
 US-08-320-157-19  
 Sequence 19, Application US/08320157  
 GENERAL INFORMATION:  
 APPLICANT: KIEFER, MICHAEL C.  
 APPLICANT: BARR, PHILIP J.  
 TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA  
 TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MORRISON & FOERSTER  
 STREET: 755 Page Mill Road  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94304-1018  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/320,157  
 FILING DATE: 07-OCT-1994  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: LEHNHARDT, SUSAN K.  
 REGISTRATION NUMBER: 33,943  
 REFERENCE/DOCKET NUMBER: 23647-20007, 20  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 813-5600  
 TELEFAX: (415) 494-0792  
 TELEX: 706141  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 280 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single



TOPOLOGY: linear  
US-08-320-157-19

Query Match 100.0%; Score 1479; DB 7; Length 280;  
Best Local Similarity 100.0%; Pred. No. 3.3e-152;  
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRCTADNSLTPAYRRRTMATGEMKEFLIGKTEPTDGINSDAQDLPSPSQAQSTRM 60  
DB 1 MTRCTADNSLTPAYRRRTMATGEMKEFLIGKTEPTDGINSDAQDLPSPSQAQSTRM 60  
QY 61 SIGESIDGKINDMEPRLDIEGFVVDYFTHIRONGMFMFGAPGLPCGVOPHEHMRVWG 120  
DB 61 SIGESIDGKINDMEPRLDIEGFVVDYFTHIRONGMFMFGAPGLPCGVOPHEHMRVWG 120  
QY 121 TIFKKHAENFETFCQDLAVPRISFLYQDVVTVGNAGTDCPMYSYGRILGISFGF 180  
DB 121 TIFKKHAENFETFCQDLAVPRISFLYQDVVTVGNAGTDCPMYSYGRILGISFGF 180  
QY 181 VAAKMMESVELQGVRLNLFVYTSLEFKTRIRNNKKEHNSWDPMFLGKQKEDYERAE 240  
DB 181 VAAKMMESVELQGVRLNLFVYTSLEFKTRIRNNKKEHNSWDPMFLGKQKEDYERAE 240  
QY 241 EKVGRKONRRMSMIGAGVTAGIGVGVVCGRMFSLK 280  
DB 241 EKVGRKONRRMSMIGAGVTAGIGVGVVCGRMFSLK 280

## RESULT 4

US-08-470-865-19  
Sequence 19, Application US/08470865  
GENERAL INFORMATION:  
APPLICANT: KIEFER, MICHAEL C.  
APPLICANT: BARR, PHILIP J.  
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA  
TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/470,865  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/320,157  
FILING DATE: 07-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: LEHNHARDT, SUSAN K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 23647-20007.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141

INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 280 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-470-865-19

Query Match 100.0%; Score 1479; DB 8; Length 280;

Best Local Similarity 100.0%; Pred. No. 3.3e-152;  
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRCTADNSLTPAYRRRTMATGEMKEFLIGKTEPTDGINSDAQDLPSPSQAQSTRM 60  
DB 1 MTRCTADNSLTPAYRRRTMATGEMKEFLIGKTEPTDGINSDAQDLPSPSQAQSTRM 60  
QY 61 SIGESIDGKINDMEPRLDIEGFVVDYFTHIRONGMFMFGAPGLPCGVOPHEHMRVWG 120  
DB 61 SIGESIDGKINDMEPRLDIEGFVVDYFTHIRONGMFMFGAPGLPCGVOPHEHMRVWG 120  
QY 121 TIFKKHAENFETFCQDLAVPRISFLYQDVVTVGNAGTDCPMYSYGRILGISFGF 180  
DB 121 TIFKKHAENFETFCQDLAVPRISFLYQDVVTVGNAGTDCPMYSYGRILGISFGF 180  
QY 181 VAAKMMESVELQGVRLNLFVYTSLEFKTRIRNNKKEHNSWDPMFLGKQKEDYERAE 240  
DB 181 VAAKMMESVELQGVRLNLFVYTSLEFKTRIRNNKKEHNSWDPMFLGKQKEDYERAE 240  
QY 241 EKVGRKONRRMSMIGAGVTAGIGVGVVCGRMFSLK 280  
DB 241 EKVGRKONRRMSMIGAGVTAGIGVGVVCGRMFSLK 280

## RESULT 5

US-08-801-248-3  
Sequence 3, Application US/08801248  
GENERAL INFORMATION:  
APPLICANT: Horvitz, H. Robert  
APPLICANT: Hengartner, Michael  
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A  
TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED  
TITLE OF INVENTION: CELL DEATH AND USES THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & RICHARDSON  
STREET: 225 Franklin Street, Suite 3100  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/801,248  
FILING DATE: 19-FEB-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/288,295  
FILING DATE: 10-AUG-1994  
APPLICATION NUMBER: US 07/927,681  
FILING DATE: 10-AUG-1992

ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 19997/201003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 280 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-801-248-3

Query Match 100.0%; Score 1479; DB 12; Length 280;

Best Local Similarity 100.0%; Pred. No. 3.3e-152;  
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSDAODLPSPSROASTRRM 60  
Db 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSDAODLPSPSROASTRRM 60  
QY 61 SIGESIDGKINDWEPRLDIEGFVVDYFTTHIRIRONGMEMFGAPGLPCGVOPHEHMMRVMG 120  
Db 61 SIGESIDGKINDWEPRLDIEGFVVDYFTTHIRIRONGMEMFGAPGLPCGVOPHEHMMRVMG 120  
QY 121 TIFEKKAENEFTECEOLLAVPRISFLYODVVRTVGNADTDCCPMSYGRLLIGLSFGGF 180  
Db 121 TIFEKKAENEFTECEOLLAVPRISFLYODVVRTVGNADTDCCPMSYGRLLIGLSFGGF 180  
QY 181 VAAKMESVELOGVARNLFVYTSLEFTRIRIRNNMKEHNSWDDEFTLTKOKMEDYERAEA 240  
Db 181 VAAKMESVELOGVARNLFVYTSLEFTRIRIRNNMKEHNSWDDEFTLTKOKMEDYERAEA 240  
QY 241 EKVGRRKQNRMSMIGAGTAGAIGIVGVVCGRRMFSLK 280  
Db 241 EKVGRRKQNRMSMIGAGTAGAIGIVGVVCGRRMFSLK 280

## RESULT 6

US-09-633-200-19  
; Sequence 19, Application US/09633200  
; GENERAL INFORMATION:  
; APPLICANT: KIEFER, MICHAEL C.  
; BARR, PHILIP J.  
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA  
; ENCODING THE PROTEINS AND METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/633,200  
; FILING DATE: 07-Aug-2000  
; CLASSIFICATION: <unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/320,157  
; FILING DATE: 07-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LEHNHARDT, SUSAN K.  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 23647-20007.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 280 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-09-633-200-19

Query Match 100.0%; Score 1479; DB 20; Length 280;  
Best Local Similarity 100.0%; Pred. No. 3.3e-152;  
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSDAODLPSPSROASTRRM 60  
Db 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSDAODLPSPSROASTRRM 60  
QY 61 SIGESIDGKINDWEPRLDIEGFVVDYFTTHIRIRONGMEMFGAPGLPCGVOPHEHMMRVMG 120  
Db 61 SIGESIDGKINDWEPRLDIEGFVVDYFTTHIRIRONGMEMFGAPGLPCGVOPHEHMMRVMG 120  
QY 121 TIFEKKAENEFTECEOLLAVPRISFLYODVVRTVGNADTDCCPMSYGRLLIGLSFGGF 180  
Db 121 TIFEKKAENEFTECEOLLAVPRISFLYODVVRTVGNADTDCCPMSYGRLLIGLSFGGF 180  
QY 181 VAAKMESVELOGVARNLFVYTSLEFTRIRIRNNMKEHNSWDDEFTLTKOKMEDYERAEA 240  
Db 181 VAAKMESVELOGVARNLFVYTSLEFTRIRIRNNMKEHNSWDDEFTLTKOKMEDYERAEA 240  
QY 241 EKVGRRKQNRMSMIGAGTAGAIGIVGVVCGRRMFSLK 280  
Db 241 EKVGRRKQNRMSMIGAGTAGAIGIVGVVCGRRMFSLK 280

## RESULT 7

US-09-791-537-10912  
; Sequence 10912, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Blonomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10912  
; LENGTH: 280  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-09-791-537-10912

Query Match 100.0%; Score 1479; DB 21; Length 280;  
Best Local Similarity 100.0%; Pred. No. 3.3e-152;  
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSDAODLPSPSROASTRRM 60  
Db 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSDAODLPSPSROASTRRM 60  
QY 61 SIGESIDGKINDWEPRLDIEGFVVDYFTTHIRIRONGMEMFGAPGLPCGVOPHEHMMRVMG 120  
Db 61 SIGESIDGKINDWEPRLDIEGFVVDYFTTHIRIRONGMEMFGAPGLPCGVOPHEHMMRVMG 120  
QY 121 TIFEKKAENEFTECEOLLAVPRISFLYODVVRTVGNADTDCCPMSYGRLLIGLSFGGF 180  
Db 121 TIFEKKAENEFTECEOLLAVPRISFLYODVVRTVGNADTDCCPMSYGRLLIGLSFGGF 180  
QY 181 VAAKMESVELOGVARNLFVYTSLEFTRIRIRNNMKEHNSWDDEFTLTKOKMEDYERAEA 240  
Db 181 VAAKMESVELOGVARNLFVYTSLEFTRIRIRNNMKEHNSWDDEFTLTKOKMEDYERAEA 240  
QY 241 EKVGRRKQNRMSMIGAGTAGAIGIVGVVCGRRMFSLK 280  
Db 241 EKVGRRKQNRMSMIGAGTAGAIGIVGVVCGRRMFSLK 280

## RESULT 8

US-09-993-420a-3  
; Sequence 3, Application US/09993420A  
; GENERAL INFORMATION:  
; APPLICANT: Horvitz, H. Robert  
; APPLICANT: Hengartner, Michael  
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A

```

; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; FILE REFERENCE: 01997/201006
; CURRENT APPLICATION NUMBER: US/09/993,420A
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 09/234,186
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 07/898,933
; PRIOR FILING DATE: 1992-06-12
; PRIOR APPLICATION NUMBER: 07/927,681
; PRIOR FILING DATE: 1992-08-10
; PRIOR APPLICATION NUMBER: 08/288,295
; PRIOR FILING DATE: 1994-08-10
; PRIOR APPLICATION NUMBER: 08/801,248
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-09-993-420a-3

```

```

Query Match          100.0%; Score 1479; DB 23; Length 280;
Best Local Similarity 100.0%; Pred. No. 3.3e-152;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADODLPSPSROASTRRM 60
   1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADODLPSPSROASTRRM 60
DB 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADODLPSPSROASTRRM 60
QY 61 SIGESIDKINDMEPRDLIEGFVVDYFTHRIKONGMEMFGAPGLPCGVOPHEHEMRVWG 120
   61 SIGESIDKINDMEPRDLIEGFVVDYFTHRIKONGMEMFGAPGLPCGVOPHEHEMRVWG 120
DB 61 SIGESIDKINDMEPRDLIEGFVVDYFTHRIKONGMEMFGAPGLPCGVOPHEHEMRVWG 120
QY 121 TFEKKHAENFETFCEDLLAVPRISFSLYODVVRVGNADQDCPMSYGRILGLISFGGF 180
   121 TFEKKHAENFETFCEDLLAVPRISFSLYODVVRVGNADQDCPMSYGRILGLISFGGF 180
DB 121 TFEKKHAENFETFCEDLLAVPRISFSLYODVVRVGNADQDCPMSYGRILGLISFGGF 180
QY 181 VAAKMMESVELOGVRNLFVYTSLFKTRIRNNMKEHNRSDDFMTLQKMKEDYERAE 240
   181 VAAKMMESVELOGVRNLFVYTSLFKTRIRNNMKEHNRSDDFMTLQKMKEDYERAE 240
DB 181 VAAKMMESVELOGVRNLFVYTSLFKTRIRNNMKEHNRSDDFMTLQKMKEDYERAE 240
QY 241 EKVGRRKRRMSMTGAGVTAGAGIAGVYVCGRMFSLK 280
   241 EKVGRRKRRMSMTGAGVTAGAGIAGVYVCGRMFSLK 280
DB 241 EKVGRRKRRMSMTGAGVTAGAGIAGVYVCGRMFSLK 280

```

```

RESULT 9
; Sequence 19, Application US/10101482
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; ENCODING THE PROTEINS AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/101,482
; FILING DATE: 18-Mar-2002
; CLASSIFICATION: <Unknown>

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
; US-10-101-482-19

```

```

Query Match          100.0%; Score 1479; DB 25; Length 280;
Best Local Similarity 100.0%; Pred. No. 3.3e-152;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADODLPSPSROASTRRM 60
   1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADODLPSPSROASTRRM 60
DB 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADODLPSPSROASTRRM 60
QY 61 SIGESIDKINDMEPRDLIEGFVVDYFTHRIKONGMEMFGAPGLPCGVOPHEHEMRVWG 120
   61 SIGESIDKINDMEPRDLIEGFVVDYFTHRIKONGMEMFGAPGLPCGVOPHEHEMRVWG 120
DB 61 SIGESIDKINDMEPRDLIEGFVVDYFTHRIKONGMEMFGAPGLPCGVOPHEHEMRVWG 120
QY 121 TFEKKHAENFETFCEDLLAVPRISFSLYODVVRVGNADQDCPMSYGRILGLISFGGF 180
   121 TFEKKHAENFETFCEDLLAVPRISFSLYODVVRVGNADQDCPMSYGRILGLISFGGF 180
DB 121 TFEKKHAENFETFCEDLLAVPRISFSLYODVVRVGNADQDCPMSYGRILGLISFGGF 180
QY 181 VAAKMMESVELOGVRNLFVYTSLFKTRIRNNMKEHNRSDDFMTLQKMKEDYERAE 240
   181 VAAKMMESVELOGVRNLFVYTSLFKTRIRNNMKEHNRSDDFMTLQKMKEDYERAE 240
DB 181 VAAKMMESVELOGVRNLFVYTSLFKTRIRNNMKEHNRSDDFMTLQKMKEDYERAE 240
QY 241 EKVGRRKRRMSMTGAGVTAGAGIAGVYVCGRMFSLK 280
   241 EKVGRRKRRMSMTGAGVTAGAGIAGVYVCGRMFSLK 280
DB 241 EKVGRRKRRMSMTGAGVTAGAGIAGVYVCGRMFSLK 280

```

```

RESULT 10
; Sequence 8, Application US/09508745
; GENERAL INFORMATION:
; APPLICANT: Cory, Suzanne
; APPLICANT: Adams, Jerry
; APPLICANT: Print, Cris
; APPLICANT: Gibson, Leonie
; APPLICANT: Koentgen, Frank
; TITLE OF INVENTION: A METHOD OF TREATMENT AND AN ANIMAL MODEL USEFUL FOR
; FILE REFERENCE: 13464
; CURRENT APPLICATION NUMBER: US/09/508,745
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: PCT/A098/00764
; PRIOR FILING DATE: 1998-09-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-508-745-8

```

```

Query Match          11.2%; Score 166; DB 19; Length 193;
Best Local Similarity 26.1%; Pred. No. 6.6e-09;
Matches 55; Conservative 28; Mismatches 90; Indels 38; Gaps 8;

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Oy 79 DIEGFVVDYFTHIRIRONGMEMFGALPCGVOPREHEMNRVMTGTFEKKHAENFETFCBOL 138  
 Db 9 DTRALVADFGVYRLRQKGYCGAGGEGPADPLHQAMRAGDEFEFRFRFTFSLAOL 68  
 Oy 139 LAVP-----RISFSIXQDVNRTVGNACIDOCMSYGRLLIGLISFGFVAAKMM--ES 188  
 Db 69 HVTGSAOQRTQVSDLEFG-----GPNMGRVAFVFGAALCAESVNREM 115  
 Oy 189 VELGOVNLVYTSLEFKTRIRNNMKRHNRSWDDFTL-GKOMKEDYERAEKVGRRK 247  
 Db 116 EPLVGQVODWIV--AYLETRILA-DWISSGGMADFTALYGDGALD-----ARRL 162  
 Oy 248 QNRKSMIGAGVTAGTIGVGVVCGRRMFS 278  
 Db 163 REGNMWASVTYVT-GAVALGALVTVGAFFAS 192

RESULT 11  
 US-09-155-327B-9  
 ; Sequence 9, Application US/09155327B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: AMRAD Operations Pty Ltd  
 ; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2  
 ; FILE REFERENCE: 2096584  
 ; CURRENT APPLICATION NUMBER: US/09/155, 327B  
 ; PRIOR APPLICATION NUMBER: P88965  
 ; PRIOR FILING DATE: 1996-03-27  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 9  
 ; LENGTH: 192  
 ; TYPE: PRT  
 ; ORGANISM: Mouse  
 US-09-155-327B-9

Query Match 10.9%; Score 161.5; DB 15; Length 192;  
 Best Local Similarity 25.6%; Pred. No. 2e-08;  
 Matches 54; Conservative 29; Mismatches 89; Indels 39; Gaps 8;  
 Oy 79 DIEGFVVDYFTHIRIRONGMEMFGALPCGVOPREHEMNRVMTGTFEKKHAENFETFCBOL 138  
 Db 9 DTRALVADFGVYRLRQKGYCGAGGEGPADPLHQAMRAGDEFEFRFRFTFSLAOL 68  
 Oy 139 LAVP-----RISFSIXQDVNRTVGNACIDOCMSYGRLLIGLISFGFVAAKMM--ES 188  
 Db 69 HVTGSAOQRTQVSDLEFG-----GPNMGRVAFVFGAALCAESVNREM 115  
 Oy 189 VELGOVNLVYTSLEFKTRIRNNMKRHNRSWDDFTL-GKOMKEDYERAEKVGRRK 247  
 Db 116 EPLVGQVODWIV--AYLETRILA-DWISSGGMADFTALYGDGALD-----ARRL 162  
 Oy 248 QNRKSMIGAGVTAGTIGVGVVCGRRMFS 278  
 Db 163 REGNMWASVTYVT-GAVALGALVTVGAFFAS 192

RESULT 12  
 PCT-US97-15872-84  
 ; Sequence 84, Application PC/TUS9715872  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KORSMEYER, STANLEY J.  
 ; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST  
 ; NUMBER OF SEQUENCES: 88  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
 ; STREET: 7733 FORSYTH BLVD., SUITE 1400  
 ; CITY: ST. LOUIS  
 ; STATE: MISSOURI  
 ; COUNTRY: USA  
 ; ZIP: 63146  
 ; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US97/15872  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/706,741  
 FILING DATE: 09-SEP-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HOLLAND, DONALD R.  
 REGISTRATION NUMBER: 35,197  
 REFERENCE/DOCKET NUMBER: 965017  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (314) 727-5188  
 TELEFAX: (314) 727-6092  
 INFORMATION FOR SEQ ID NO: 84:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 27 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 PCT-US97-15872-84

Query Match 10.5%; Score 156; DB 1; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-09;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 73 WEPRLDIEGFVVDYFTHIRIRONGMEM 99  
 Db 1 WEPRLDIEGFVVDYFTHIRIRONGMEM 27

RESULT 13  
 US-08-706-741-84  
 ; Sequence 84, Application US/08706741  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KORSMEYER, STANLEY J.  
 ; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST  
 ; NUMBER OF SEQUENCES: 88  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
 ; STREET: 7733 FORSYTH BLVD., SUITE 1400  
 ; CITY: ST. LOUIS  
 ; STATE: MISSOURI  
 ; COUNTRY: USA  
 ; ZIP: 63146  
 ; COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/706,741  
 FILING DATE:  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HOLLAND, DONALD R.  
 REGISTRATION NUMBER: 35,197  
 REFERENCE/DOCKET NUMBER: 965017  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (314) 727-5188  
 TELEFAX: (314) 727-6092  
 INFORMATION FOR SEQ ID NO: 84:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 27 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide

US-08-706-741-84

Query Match 10.5%; Score 156; DB 11; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-09;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 73 WEPRDIEGFVVDYFTHIRONGMEW 99  
 ||||||||||||||||||  
 Db 1 WEPRDIEGFVVDYFTHIRONGMEW 27

RESULT 14

US-08-706-741A-84  
 ; Sequence 84, Application US/08706741A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KORSMEYER, STANLEY J.  
 ; TITLE OF INVENTION: B33 INTERACTING DOMAIN DEATH AGONIST  
 ; NUMBER OF SEQUENCES: 88  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
 ; STREET: 7733 FORSYTH BLVD., SUITE 1400  
 ; CITY: ST. LOUIS  
 ; STATE: MISSOURI  
 ; COUNTRY: USA  
 ; ZIP: 63146  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/706,741A  
 ; FILING DATE:  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: HOLLAND, DONALD R.  
 ; REGISTRATION NUMBER: 35,197  
 ; REFERENCE/DOCKET NUMBER: 965017  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (314) 727-5188  
 ; TELEFAX: (314) 727-6092  
 ; INFORMATION FOR SEQ. ID NO.: 84:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 27 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-706-741A-84

Query Match 10.5%; Score 156; DB 11; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-09;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 73 WEPRDIEGFVVDYFTHIRONGMEW 99  
 ||||||||||||||||||  
 Db 1 WEPRDIEGFVVDYFTHIRONGMEW 27

RESULT 15

US-08-733-505-49  
 ; Sequence 49, Application US/08733505  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KORSMEYER, STANLEY J.  
 ; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF  
 ; NUMBER OF SEQUENCES: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
 ; STREET: 7733 FORSYTH BLVD., SUITE 1400  
 ; CITY: ST. LOUIS  
 ; STATE: MISSOURI  
 ; COUNTRY: USA

ZIP: 63105  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/733,505  
 ; FILING DATE:  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: HOLLAND, DONALD R.  
 ; REGISTRATION NUMBER: 35,197  
 ; REFERENCE/DOCKET NUMBER: 965458  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (314) 727-5188  
 ; TELEFAX: (314) 727-6092  
 ; INFORMATION FOR SEQ. ID NO.: 49:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 27 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-733-505-49

Query Match 10.5%; Score 156; DB 11; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-09;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 73 WEPRDIEGFVVDYFTHIRONGMEW 99  
 ||||||||||||||||||  
 Db 1 WEPRDIEGFVVDYFTHIRONGMEW 27

Search completed: February 24, 2003, 11:57:57  
 Job time : 146 secs

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•  
•  
•

GenCore version 5.1.3  
(c) 1993 - 2003 CompuGen Ltd

OM protein - protein search, using sw model

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Run on:      February 24, 2003, 11:54:04 ; Search time 59 Seconds
              (without alignments)
              428.745 Million cell updates/sec
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Title:	US-09-993-420A-3
Perfect score:	1479
Sequence:	1 MTRCTADNSLTNPAYRRRTM.....AGATGIVGVVCGRMPSLK 280

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473410 seqs, 90342619 residues

Total number of hits satisfying chosen parameters: 473416

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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	Database
1:	pending_patents_AA_Near *
2:	/cgn2.6/pdata1.1/paa/PCIT_NEW_COMB.pcp *
3:	/cgn2.6/pdata1.1/paa/US06_NEW_COMB.pcp *
4:	/cgn2.6/pdata1.1/paa/US07_NEW_COMB.pcp *
5:	/cgn2.6/pdata1.1/paa/US08_NEW_COMB.pcp *
6:	/cgn2.6/pdata1.1/paa/US09_NEW_COMB.pcp *
7:	/cgn2.6/pdata1.1/paa/US10_NEW_COMB.pcp *
8:	/cgn2.6/pdata1.1/paa/US16_NEW_COMB.pcp *

**pred.** No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	712.5	48.2	137	5	US-09-155-327G-15	Sequence 15, Appl
2	712.5	48.2	137	5	US-09-155-327F-15	Sequence 15, Appl
3	154	10.4	193	5	US-09-155-327G-9	Sequence 9, Appl
4	154	10.4	193	5	US-09-155-327F-9	Sequence 9, Appl
5	150	10.1	193	5	US-09-155-337G-7	Sequence 7, Appl
6	150	10.1	193	5	US-09-155-327F-7	Sequence 7, Appl
7	138	9.3	233	6	US-10-049-822A-3	Sequence 3, Appl
8	136	9.2	333	5	US-09-155-327G-10	Sequence 10, Appl
9	136	9.2	333	5	US-09-155-327F-10	Sequence 10, Appl
10	135	9.1	233	5	US-09-155-327G-12	Sequence 12, Appl
11	135	9.1	233	5	US-09-155-327F-12	Sequence 12, Appl
12	135	9.1	233	6	US-10-049-822A-2	Sequence 2, Appl
13	135	9.1	233	6	US-10-307-262-2	Sequence 2, Appl
14	135	9.1	233	6	US-10-168-223-10	Sequence 10, Appl
15	126.5	8.6	212	6	US-10-169-223-14	Sequence 14, Appl
16	126	8.5	365	5	US-09-010-147B-24	Sequence 24, Appl
17	116	7.8	365	6	US-10-314-942-24	Sequence 24, Appl
18	116	7.8	339	5	US-09-155-327G-11	Sequence 11, Appl
19	116	7.8	239	5	US-09-155-327F-11	Sequence 11, Appl
20	116	7.8	239	6	US-10-277-693A-10	Sequence 10, Appl
21	113.5	7.7	236	6	US-10-277-693A-11	Sequence 11, Appl
22	108	7.1	20	6	US-10-167-223-9	Sequence 9, Appl
23	105.5	7.3	99	6	US-10-294-445-26	Sequence 26, Appl
24	100	6.8	203	6	US-10-236-392-18	Sequence 18, Appl
25	100	6.8	222	6	US-10-236-397-16	Sequence 16, Appl
26	98.5	6.7	216	6	US-10-236-392-14	Sequence 14, Appl

## ALIGNMENTS

27	95	6.4	350	6	US-10-236-332-12	Sequence 12, App1
28	90	6.1	274	6	US-10-287-274-369	Sequence 369, App
29	90	6.1	274	6	US-10-287-274-407	Sequence 407, App
30	83	5.6	516	6	US-10-212-766-24	Sequence 24, App1
31	83	5.6	516	6	US-09-950-084-5147	Sequence 5147, Ap
32	83	5.4	385	5	US-09-724-676-85980	Sequence 85980, A
33	80	5.4	385	5	US-09-724-676-85980	Sequence 85980, A
34	80	5.4	385	5	US-09-724-676A-85994	Sequence 85994, A
35	80	5.4	395	5	US-09-724-676A-85994	Sequence 85994, A
36	80	5.4	529	5	US-09-724-676A-85992	Sequence 85992, A
37	80	5.4	529	5	US-09-724-676A-85992	Sequence 85992, A
38	80	5.4	529	5	US-09-935-145A-25	Sequence 6, App1
39	80	5.4	529	5	US-10-214-766-25	Sequence 25, App1
40	78.5	5.3	639	6	US-10-302-267-8	Sequence 8, App1
41	78	5.3	512	6	US-10-181-663-16	Sequence 16, App1
42	77.5	5.2	338	6	US-10-214-766-23	Sequence 23, App
43	77.5	5.2	376	5	US-09-950-084-4544	Sequence 4544, App
44	77.5	5.2	418	6	US-10-301-822-187	Sequence 187, App
45	76.5	5.2	99	6	US-10-294-445-27	Sequence 27, App1

## RESULT 1

```

US-09-153-327G-15
: Sequence 15, Application US/09155327G
: GENERAL INFORMATION:
: APPLICANT: ARAD Operations Pty Ltd
: TITLE OF INVENTION: A NOVEL, MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
: TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
: FILE REFERENCE: 2096584
: CURRENT APPLICATION NUMBER: US/09/155,327G
: CURRENT FILING DATE: 1999-03-29
: PRIOR APPLICATION NUMBER: P8965
: PRIOR FILING DATE: 1996-05-27
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 15
: LENGTH: 137
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-153-327G-15

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Query Match	48.28;	Score 712.5;	DB 5;	Length 137;
Best Local Similarity	91.3%;	Pred. No. 2.3e-65;		
Matches 137;	Conservative	0;	Mismatches 0;	Indels 13;
				Gaps 1

Qy	79	DIEEFVVDYTHHIRONGHEWGAAGLDCGOFHEHEMRWGLIFAKRINENL	137
Db	1	DIEEFVVDYTHHIRONGHEW-----HEHEMRWGLIFEKKAHENEFTFCQL	47
Qy	139	LAVRISFSLYOQVVPVFNNAOTDCCPMYSRGLIGLSIFGCFVAAKMSVBLQGVNLT	196
Db	48	LAVRISFSLXQVAVTVGNAOTDCCPMYSRGLIGLSIFGCFVAAKMSVESLQGVNLT	107
Qy	199	FVYTSLSFIKTRIRNNKKEHNRSMDFPRLG	228
Db	108	FVYTSLSFIKTRIRNNKKEHNRSMDFPRLG	137

## RESULT

```

US-09-135-32/F-15
; Sequence 15, Application US/09155327F
;
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
; FILE REFERENCE: 2096584
; CURRENT APPLICATION NUMBER: US/09/155,327F
; CURRENT FILING DATE: 1996-03-27
; PRIOR APPLICATION NUMBER: PN8965
; PRIOR FILING DATE: 1996-03-27

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; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 15
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-155-327F-15

```

```

Query Match
Best Local Similarity 48.2%; Score 712.5; DB 5; Length 137;
Matches 137; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

```

```

QY 79 DIEGFVVDYFTHRIKRONGMEWFGAPGLPCGVQPEHEMRYMGTIFEKKHAENFEFCEOL 138
DB 1 DIEGFVVDYFTHRIKRONGMEW-----HEMRYMGTIFEKKHAENFEFCEOL 47
QY 139 LAVPRISFSLYQDVYRTVGNAGTDCPMSYGRILGISFGFVAAMMESVELQGVNRL 198
DB 48 LAVPRISFSLYQDVYRTVGNAGTDCPMSYGRILGISFGFVAAMMESVELQGVNRL 107
QY 199 FVTSLSFKTRIRNNKKEHNSWDDPMTLG 228
DB 108 FVTSLSFKTRIRNNKKEHNSWDDPMTLG 137

```

## RESULT 3

```

US-09-155-327G-9
; Sequence 9, Application US/09155327G
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
; FILE REFERENCE: 2096584
; CURRENT APPLICATION NUMBER: US/09/155,327G
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PN8965
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Mouse
US-09-155-327G-9

```

```

Query Match
Best Local Similarity 10.4%; Score 154; DB 5; Length 193;
Matches 52; Conservative 30; Mismatches 92; Indels 36; Gaps 8;

```

```

QY 79 DIEGFVVDYFTHRIKRONGMEWFGAPGLPCGVQPEHEMRYMGTIFEKKHAENFEFCEOL 138
DB 9 DTRALVADVFVGYRLKOKGYCGAGPGECPADPLHQAMRAAGDEFETRFRRTESDLAOL 68
QY 139 LAVP-----RISFSLYQDVYRTVGNAGTDCPMSYGRILGISFGFVAAMM--ES 188
DB 69 HVTGSAOQRTQVSDLEFQG-----GPNMGRVAFVFGALCAESVKNEM 115
QY 189 VELQGOVRLNLFVYTSLFKTRIRNNKKEHNSWDDPMTLGOKMEDYERAEAEVGRRKQ 248
DB 116 EPLVGQVQDMWV---ATLETRLA-DWTHSSGMAEFETAL-----YGDALBE-ARRLR 163
QY 249 NRRSMIGAGVTAGAGTIGVGVCGRMMS 278
DB 164 EGNWASVRT-VLTGVALGALVTYGAFFAS 192

```

## RESULT 4

```

US-09-155-327F-9
; Sequence 9, Application US/09155327F
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
; FILE REFERENCE: 2096584
; CURRENT APPLICATION NUMBER: US/09/155,327F
; PRIOR FILING DATE: 1999-03-27
; PRIOR APPLICATION NUMBER: PN8965
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Mouse
US-09-155-327F-9

```

```

; FILE REFERENCE: 2096584
; CURRENT APPLICATION NUMBER: US/09/155,327F
; CURRENT FILING DATE: 1996-03-27
; PRIOR APPLICATION NUMBER: PN8965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Mouse
US-09-155-327F-9

```

```

Query Match
Best Local Similarity 10.4%; Score 154; DB 5; Length 193;
Matches 52; Conservative 30; Mismatches 92; Indels 36; Gaps 8;

```

```

QY 79 DIEGFVVDYFTHRIKRONGMEWFGAPGLPCGVQPEHEMRYMGTIFEKKHAENFEFCEOL 138
DB 9 DTRALVADVFVGYRLKOKGYCGAGPGECPADPLHQAMRAAGDEFETRFRRTESDLAOL 68
QY 139 LAVP-----RISFSLYQDVYRTVGNAGTDCPMSYGRILGISFGFVAAMM--ES 188
DB 69 HVTGSAOQRTQVSDLEFQG-----GPNMGRVAFVFGALCAESVKNEM 115
QY 189 VELQGOVRLNLFVYTSLFKTRIRNNKKEHNSWDDPMTLGOKMEDYERAEAEVGRRKQ 248
DB 116 EPLVGQVQDMWV---ATLETRLA-DWTHSSGMAEFETAL-----YGDALBE-ARRLR 163
QY 249 NRRSMIGAGVTAGAGTIGVGVCGRMMS 278
DB 164 EGNWASVRT-VLTGVALGALVTYGAFFAS 192

```

## RESULT 5

```

US-09-155-327G-7
; Sequence 7, Application US/09155327G
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
; FILE REFERENCE: 2096584
; CURRENT APPLICATION NUMBER: US/09/155,327G
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PN8965
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 193
; TYPE: PRT
; ORGANISM: HUMAN
US-09-155-327G-7

```

```

Query Match
Best Local Similarity 10.1%; Score 150; DB 5; Length 193;
Matches 51; Conservative 30; Mismatches 93; Indels 36; Gaps 8;

```

```

QY 79 DIEGFVVDYFTHRIKRONGMEWFGAPGLPCGVQPEHEMRYMGTIFEKKHAENFEFCEOL 138
DB 9 DTRALVADVFVGYRLKOKGYCGAGPGECPADPLHQAMRAAGDEFETRFRRTESDLAOL 68
QY 139 LAVP-----RISFSLYQDVYRTVGNAGTDCPMSYGRILGISFGFVAAMM--ES 188
DB 69 HVTGSAOQRTQVSDLEFQG-----GPNMGRVAFVFGALCAESVKNEM 115
QY 189 VELQGOVRLNLFVYTSLFKTRIRNNKKEHNSWDDPMTLGOKMEDYERAEAEVGRRKQ 248
DB 116 EPLVGQVQDMWV---ATLETRLA-DWTHSSGMAEFETAL-----YGDALBE-ARRLR 163
QY 249 NRRSMIGAGVTAGAGTIGVGVCGRMMS 278
DB 164 EGNWASVRT-VLTGVALGALVTYGAFFAS 192

```





SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 10  
LENGTH: 333  
TYPE: PRT  
ORGANISM: murine  
US-09-155-327F-10

Query Match 9.1%; Score 136; DB 5; Length 333;  
Best Local Similarity 23.5%; Pred. No. 1.2e-05;  
Matches 46; Conservative 34; Mismatches 88; Indels 28; Gaps 6;

QY 79 DIEFVVDYFTHIRIRONGMEWFGAPGLPCGVQVPEHEMRVWGTIFECQQLAVPRIISFLYQDVYR 138  
DB 9 DTRALVADFGVYKLRQKGYVCGAGCPADPLHQAMRAAGDEFFTRFRRTFSDLAQL 68  
QY 139 LAVP-----RISFLYQDVYRTVGNQTDCCPMSTGRILIGLISFGFVAAKMM--ES 188  
DB 69 HVPFGSAQQRFTQVSDLLFG-----GPMWGLVAFVFPVGAALCAESVAKEM 115  
QY 189 VELQGVNLFVYTSLFIFKIRIRNNKEHNRSMDDFTLQKMKEDYERAEKVRKQ 248  
DB 116 EPLVGGVQDDMVV--AYLETRLA-DWIHSSGGW-ELEAIKARVEMEEAEKLEIQNEV 170  
QY 249 NRKSMIGAGVTAIGAI 264  
DB 171 EKQNMSPPGNAGPV 186

RESULT 10  
US-09-155-327G-12  
Sequence 12, Application US/09155327G  
GENERAL INFORMATION:  
APPLICANT: AMRAD Operations Pty Ltd  
TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2  
FAMILY OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES  
FILE REFERENCE: 2096584  
CURRENT APPLICATION NUMBER: US/09/155,327G  
CURRENT FILING DATE: 1999-03-29  
PRIOR APPLICATION NUMBER: PN8965  
PRIOR FILING DATE: 1996-03-27  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 12  
LENGTH: 233  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-155-327G-12

Query Match 9.1%; Score 135; DB 5; Length 233;  
Best Local Similarity 21.3%; Pred. No. 9.4e-06;  
Matches 53; Conservative 38; Mismatches 82; Indels 76; Gaps 10;

QY 84 VVDYFTHIRIRONGMEWFGAPGLPCGVQVPEHE----- 114  
DB 9 VVDYFTHIRIRONGMEWFGAPGLPCGVQVPEHE----- 114  
QY 115 -----MMRWGTIFECQQLAVPRIISFLYQDVYR 154  
DB 69 TGHSSSLDAREVYIPMAAVKQALREAGDEFFELRYRAFSDLTSQLHTTPTAVQSPQVYN 128  
QY 155 TVGNQTDCCPMSTGRILIGLISFGFVAAKMMESV--ELQGVNLFVYTSLFIFKIRIRN 212  
DB 129 -----ELFRDGVNMRIRIAYFSSFG--ALCVESYDKRMQVLSRIAAMATYIINDHL-E 179  
QY 213 NMKEHNRSMDDFTLQKMKEDY-ERAEAEKVRGRKRRNSMIGAGVTAIGIVGVV 271  
DB 180 PVIQENGMDTFVEL-----YGNNAAEESRKQGERFRNFWELTG-----MTVAGVVL 225  
QY 272 CGRMWFSLK 280  
DB 226 LG-SLFSRK 233

RESULT 11  
US-09-155-327F-12  
Sequence 12, Application US/09155327F  
GENERAL INFORMATION:  
APPLICANT: AMRAD Operations Pty Ltd  
TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2  
FAMILY OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES  
FILE REFERENCE: 2096584  
CURRENT APPLICATION NUMBER: US/09/155,327F  
CURRENT FILING DATE: 1996-03-27  
PRIOR APPLICATION NUMBER: PN8965  
PRIOR FILING DATE: 1996-03-27  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 12  
LENGTH: 233  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-155-327F-12

Query Match 9.1%; Score 135; DB 5; Length 233;  
Best Local Similarity 21.3%; Pred. No. 9.4e-06;  
Matches 53; Conservative 38; Mismatches 82; Indels 76; Gaps 10;

QY 84 VVDYFTHIRIRONGMEWFGAPGLPCGVQVPEHE----- 114  
DB 9 VVDYFTHIRIRONGMEWFGAPGLPCGVQVPEHE----- 114  
QY 115 -----MMRWGTIFECQQLAVPRIISFLYQDVYR 154  
DB 69 TGHSSSLDAREVYIPMAAVKQALREAGDEFFELRYRAFSDLTSQLHTTPTAVQSPQVYN 128  
QY 155 TVGNQTDCCPMSTGRILIGLISFGFVAAKMMESV--ELQGVNLFVYTSLFIFKIRIRN 212  
DB 129 -----ELFRDGVNMRIRIAYFSSFG--ALCVESYDKRMQVLSRIAAMATYIINDHL-E 179  
QY 213 NMKEHNRSMDDFTLQKMKEDY-ERAEAEKVRGRKRRNSMIGAGVTAIGIVGVV 271  
DB 180 PVIQENGMDTFVEL-----YGNNAAEESRKQGERFRNFWELTG-----MTVAGVVL 225  
QY 272 CGRMWFSLK 280  
DB 226 LG-SLFSRK 233

RESULT 12  
US-10-049-822A-2  
Sequence 2, Application US/10049822A  
GENERAL INFORMATION:  
APPLICANT: ONTQA, Shigeo  
TITLE OF INVENTION: A GENETICALLY ENGINEERED CDNA OF RAT bcl-x GENE AND AN IMPROVE  
FILE REFERENCE: 2002-0256A/C/00653  
CURRENT APPLICATION NUMBER: US/10/049,822A  
CURRENT FILING DATE: 2002-04-01  
PRIOR APPLICATION NUMBER: PCT/JP00/05502  
PRIOR FILING DATE: 2000-08-17  
PRIOR APPLICATION NUMBER: JP11-230642  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 233  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
US-10-049-822A-2

Query Match 9.1%; Score 135; DB 6; Length 233;  
Best Local Similarity 21.3%; Pred. No. 9.4e-06;  
Matches 53; Conservative 38; Mismatches 82; Indels 76; Gaps 10;

QY 84 VVDYFTHIRIRONGMEWFGAPGLPCGVQVPEHE----- 114  
DB 9 VVDYFTHIRIRONGMEWFGAPGLPCGVQVPEHE----- 114

Db 9 VVDFLSYKLSQKGYWSQFSVDEENRTAEPEERETPSAINGNPSWHLADSPAVNGA 68  
QY 115 -----MMRVMTGTFEKKHAENFETCEOLLAVPRISFSLYODVVR 154  
Db 69 TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTTPTGTAQSFQVYN 128  
QY 155 TVGNAQTDQCPMSYGRLLIGLISFGGFVAAKMESV--ELQGVNRLFYVTSLFITRIRN 212  
Db 129 -----ELFRDGVNMGRIYVAFSPFG--ALCVESYDKEMQVLSRIASMAATYLDNHL-E 179  
QY 213 NKEHNRSWDEFTLGRKQKEDY-ERAEAEKVGRRKQNRKMSMIGAGVTAGATGIVGVV 271  
Db 180 PWIDENGMDTFEVL-----YGNMAAESRKQGERFNMFLTG-----MTVAGVVL 225  
QY 272 CGRMFSLK 280  
Db 226 LG-SLFSRK 233

RESULT 13  
US-10-302-262-2  
; Sequence 2, Application US/10302262  
; GENERAL INFORMATION:  
; APPLICANT: Benmett, C. Frank  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Nickoloff, Brian J.  
; APPLICANT: Zhang, Qiongling  
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
; FILE REFERENCE: ISPh-0528  
; CURRENT APPLICATION NUMBER: US/10/302,262  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US/09/734,846  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 09/277,020  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 09/167,921  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 09/323,743  
; PRIOR FILING DATE: 1999-06-02  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 233  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
US-10-302-262-2

Query Match 9.1%; Score 135; DB 6; Length 233;  
Best Local Similarity 21.3%; Pred. No. 9.4e-06;  
Matches 53; Conservative 38; Mismatches 82; Indels 76; Gaps 10;

QY 84 VVDYFTHIRONGMEWF-----GAPGLPCGVOPRHE----- 114  
Db 9 VVDFLSYKLSQKGYWSQFSVDEENRTAEPEERETPSAINGNPSWHLADSPAVNGA 68  
QY 115 -----MMRVMTGTFEKKHAENFETCEOLLAVPRISFSLYODVVR 154  
Db 69 TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTTPTGTAQSFQVYN 128  
QY 155 TVGNAQTDQCPMSYGRLLIGLISFGGFVAAKMESV--ELQGVNRLFYVTSLFITRIRN 212  
Db 129 -----ELFRDGVNMGRIYVAFSPFG--ALCVESYDKEMQVLSRIASMAATYLDNHL-E 179  
QY 213 NKEHNRSWDEFTLGRKQKEDY-ERAEAEKVGRRKQNRKMSMIGAGVTAGATGIVGVV 271  
Db 180 PWIDENGMDTFEVL-----YGNMAAESRKQGERFNMFLTG-----MTVAGVVL 225  
QY 272 CGRMFSLK 280  
Db 226 LG-SLFSRK 233

RESULT 14  
US-10-169-223-10  
; Sequence 10, Application US/10169223  
; GENERAL INFORMATION:  
; APPLICANT: Shimizu, Shigeomi  
; APPLICANT: TSUTIMOTO, Yoshihide  
; TITLE OF INVENTION: BH4-Fused Polypeptides  
; FILE REFERENCE: 1422-0537P  
; CURRENT APPLICATION NUMBER: US/10/169,223  
; CURRENT FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: JP 11-371449  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: PCT/JP00/09274  
; PRIOR FILING DATE: 2000-12-26  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 233  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
US-10-169-223-10

Query Match 9.1%; Score 135; DB 6; Length 233;  
Best Local Similarity 21.3%; Pred. No. 9.4e-06;  
Matches 53; Conservative 38; Mismatches 82; Indels 76; Gaps 10;

QY 84 VVDYFTHIRONGMEWF-----GAPGLPCGVOPRHE----- 114  
Db 9 VVDFLSYKLSQKGYWSQFSVDEENRTAEPEERETPSAINGNPSWHLADSPAVNGA 68  
QY 115 -----MMRVMTGTFEKKHAENFETCEOLLAVPRISFSLYODVVR 154  
Db 69 TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTTPTGTAQSFQVYN 128  
QY 155 TVGNAQTDQCPMSYGRLLIGLISFGGFVAAKMESV--ELQGVNRLFYVTSLFITRIRN 212  
Db 129 -----ELFRDGVNMGRIYVAFSPFG--ALCVESYDKEMQVLSRIASMAATYLDNHL-E 179  
QY 213 NKEHNRSWDEFTLGRKQKEDY-ERAEAEKVGRRKQNRKMSMIGAGVTAGATGIVGVV 271  
Db 180 PWIDENGMDTFEVL-----YGNMAAESRKQGERFNMFLTG-----MTVAGVVL 225  
QY 272 CGRMFSLK 280  
Db 226 LG-SLFSRK 233

RESULT 15  
US-10-169-223-14  
; Sequence 14, Application US/10169223  
; GENERAL INFORMATION:  
; APPLICANT: SHIMIZU, Shigeomi  
; APPLICANT: TSUTIMOTO, Yoshihide  
; TITLE OF INVENTION: BH4-Fused Polypeptides  
; FILE REFERENCE: 1422-0537P  
; CURRENT APPLICATION NUMBER: US/10/169,223  
; CURRENT FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: JP 11-371449  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: PCT/JP00/09274  
; PRIOR FILING DATE: 2000-12-26  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 212  
; TYPE: PRF  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: CDS of Synthesized DNA for mutant bcl-xL  
US-10-169-223-14

Query Match 8.6%; Score 126.5; DB 6; Length 212;  
Best Local Similarity 25.3%; Pred. No. 6.1e-05;

	Matches	43;	Conservative	33;	Mismatches	67;	Indels	27;	Gaps	8;	
QY	114	EMKRVNGTIF	EKKHAENETFC	EQLLAVPRIS	SLYQDVVRY	GNNAQTDC	PMSTYGR	LIG	173		
DB	67	QALREAGDE	FEELRYRRA	FSDLTSQ	LHITPGTAY	QSEQVYN	----	ELFRDGVN	WGRIVA	121	
QY	174	LTSFGGEV	AAKMMESY	-ELOGOV	RNLFVYTS	SLFIKTR	RNNMKEH	NRSDDE	FMTLGK	231	
DB	122	FFSFGG	---	ALCVESY	DKENQV	LSRIA	MMATY	LNDHL	-EPWIQENG	MDTEVEL	173
QY	232	KEDY	-E	RAEA	EKVGR	RRKQNR	MSMIG	AGVTAG	AIGIV	GVVCGRM	280
DB	174	---	YGNNA	AAESR	KQGR	ENRWF	LTG	-----	MTVAGV	VLLG	212

Search completed: February 24, 2003, 11:59:02  
 Job time : 59 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 24, 2003, 11:52:39 ; Search time 18 Seconds  
(without alignments)  
1495.424 Million cell updates/sec

Title: US-09-993-420a-3

Perfect score: 1479  
Sequence: 1 MTRCTADNSLTNPAYRRRRM.....ACATGIVGVVCGMMFSLK 280

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.73:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1479	100.0	280	2	A53189 apoptosis suppressor protein ced-9 (imp
2	1377	93.1	261	2	H88578 apoptosis regulator
3	135	9.1	233	2	B47537 BCL-X protein - ra
4	135	9.1	233	2	S51761 bcl-x long - mouse
5	132	8.9	233	2	I49056 BCL-X long - rat
6	126	8.5	233	2	I67431 transforming prote
7	116	7.8	233	2	A37332 transforming prote
8	116	7.8	239	1	TVH041 transforming prote
9	113.5	7.7	236	1	TVWSA1 BCL-2 - rat (fragm
10	113.5	7.7	236	1	I67432 NR-13 protein - qu
11	112	7.6	177	2	SC4778 B-cell lymphoma 2
12	110.5	7.5	236	2	IC7383 gene bcl-2 protein
13	109.5	7.4	236	2	I53744 bcl-x transmembran
14	108	7.3	214	2	I49057 WD-repeat containi
15	108	7.3	1329	2	AE1901 transactivating pro
16	106.5	7.2	232	2	S24390 apoptosis regulator
17	99	6.7	227	2	JE0203 hypothetical prote
18	96.5	6.5	757	2	F83516 transforming prote
19	95	6.4	199	1	TVWSB1 BCL2 homolog MCL1
20	95	6.4	350	2	A47476 transforming prote
21	94.5	6.4	216	2	B37332 transactivating pro
22	90.5	6.1	205	1	TVH0B1 hypothetical prote
23	90.5	6.1	279	2	H90992 thiamin biosynthes
24	90.5	6.1	607	2	AH2891 thiamin biosynthes
25	90.5	6.1	644	2	D97667 hypothetical prote
26	90	6.1	274	2	A64978 probable phosphoe
27	89.5	6.0	1217	2	F69823 apoptosis regulato
28	89	6.0	190	2	A47537 hypothetical prote
29	88.5	6.0	283	2	C85838

30	88	5.9	255	2	JC7567 Mcl-1a protein - 2
31	88	5.9	436	2	S13583 nosd protein precu
32	87	5.9	347	2	S35229 hypd' protein - Br
33	86	5.8	384	2	D86821 hydroxymethylgluta
34	85	5.7	1737	2	A57491 hypothetical heli
35	84.5	5.7	150	2	D81356 methylated-DNA-lpr
36	84.5	5.7	430	2	H83178 conserved hypotet
37	84	5.7	383	2	H98287 hypothetical prote
38	83.5	5.6	1657	2	T15838 hypothetical prote
39	83	5.6	361	2	A65050 membrane-bound lyl
40	83	5.6	316	1	XDPJVS 3-phosphoshikimate
41	83	5.6	545	2	B89823 hypothetical prote
42	83	5.6	1112	2	H95964 probable outer mem
43	82.5	5.6	447	2	JC5352 2-nitrofluorene dio
44	82.5	5.6	574	2	T16230 hypothetical prote
45	82.5	5.6	608	2	T51217 hypothetical prote

#### ALIGNMENTS

##### RESULT 1

A53189 apoptosis suppressor CED-9 - Caenorhabditis elegans  
N:Alternate names: hypothetical protein T07C4.8; proto-oncogene bcl-2 homolog  
C:Species: Caenorhabditis elegans  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jul-2000  
C:Accession: A53189; S41021  
R:Hengartner, M.O.; Horvitz, H.R.  
Cell 76, 665-676, 1994  
A:Title: Caenorhabditis elegans cell survival gene ced-9 encodes a functional homolog  
A:Reference number: A53189; MUID:94170367; PMID:7907274  
A:Accession: A53189  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-280 <HEND>  
A:Cross-references: GB:L26545; NID:9433174; PIDN:AAA20080.1; PID:9433176  
R:Berts, M.  
submitted to the EMBL Data Library, January 1994  
A:Reference number: S41014  
A:Accession: S41021  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 20-280 <BER>  
A:Cross-references: EMBL:Z29443; NID:91067051; PID:9443835  
C:Genetics:  
A:Gene: ced-9  
A:Introns: 84/3; 171/3; 22/3

Query Match	Similarity	Score	1479;	DB 2;	Length	280;			
Best Local	100.0%;	Pred. No.	2.6e-129;						
Matches	280;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0
QY	1	MTRCTADNSLTNPAYRRRRMATGEMKEFLGKGPEDFGINSADQDLPSPROASTRRM	60						
DB	1	MTRCTADNSLTNPAYRRRRMATGEMKEFLGKGPEDFGINSADQDLPSPROASTRRM	60						
QY	61	STGESIDCKINDWEPRLDIEGFVVDYFTFHRIRONGEMEGAPGLPCGVOPPEHMMRVMG	120						
DB	61	STGESIDCKINDWEPRLDIEGFVVDYFTFHRIRONGEMEGAPGLPCGVOPPEHMMRVMG	120						
QY	121	TIIEKKHAENFEFCEDLLAVPRISFSLYODVFTVGNADTDCPMYGRILGISGGR	180						
DB	121	TIIEKKHAENFEFCEDLLAVPRISFSLYODVFTVGNADTDCPMYGRILGISGGR	180						
QY	181	VAAKMSEVEIQGVNRNLFVYTSLEIKTRIRNNMKEHNRSDDEMTLGKMKEDYEAAE	240						
DB	181	VAAKMSEVEIQGVNRNLFVYTSLEIKTRIRNNMKEHNRSDDEMTLGKMKEDYEAAE	240						
QY	241	EKVGRRKONRRSMIGAGVTAGTAGIIVGVVCGMMFSLK	280						
DB	241	EKVGRRKONRRSMIGAGVTAGTAGIIVGVVCGMMFSLK	280						

RESULT 2  
 H88578  
 protein ced-9 [imported] - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
 C:Accession: H88578  
 R:Anonymous, The C. elegans Sequencing Consortium.  
 Science 283, 2012-2018, 1998  
 A>Title: Genome sequence of the nematode C. elegans: a platform for investigating biology  
 A:Reference number: A75000; MUID:99069613; PMID:9851916  
 A:Note: see webstiles genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.ela  
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
 A:Accession: H88578  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-261 <STO>  
 A:Cross-references: GB:chr\_III; PIDN:CAA82573.1; PID:g3879511; GSPDB:GN00021  
 C:Genetics:  
 A:Gene: ced-9  
 A:Map position: 3

Query Match 93.1%; Score 1377; DB 2; Length 261;  
 Best Local Similarity 100.0%; Pred. No. 6,7e-120;  
 Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 MATGEMKEFLGKTEPTDFGINSADADLPSPROASTRMSIGESTIDGKINDEPRD 79  
 |||||  
 Db 1 MATGEMKEFLGKTEPTDFGINSADADLPSPROASTRMSIGESTIDGKINDEPRD 60  
 QY 80 IEGFVVDYFTHIRIRONGMEMFGAPGCGVOPHEHMRVAGTTFEKKHAENFTFCEOLL 139  
 |||||  
 Db 61 IEGFVVDYFTHIRIRONGMEMFGAPGCGVOPHEHMRVAGTTFEKKHAENFTFCEOLL 120  
 QY 140 AVPRISLSLQDVPRVGNAGTQCCMSYGRLLIGLISFGGFVAAKMESVEIQQVRLNF 199  
 |||||  
 Db 121 AVPRISLSLQDVPRVGNAGTQCCMSYGRLLIGLISFGGFVAAKMESVEIQQVRLNF 180  
 QY 200 VYTSLEFKTRIRNNKKEHNSMDPMTLGKOMEDEYERAEKVGRRKRRMSMGAGV 259  
 |||||  
 Db 181 VYTSLEFKTRIRNNKKEHNSMDPMTLGKOMEDEYERAEKVGRRKRRMSMGAGV 240  
 QY 260 TAGATGIVGVVCGRRMFSLK 280  
 |||||  
 Db 241 TAGATGIVGVVCGRRMFSLK 261

## RESULT 3

B47537  
 apoptosis regulator bcl-xl - human  
 N:Alternate names: bcl-2-related protein  
 N:Contains: apoptosis regulator bcl-xs  
 C:Species: Homo sapiens (man)  
 C:Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 16-Jul-1999  
 C:Accession: B47537; C47537  
 R:Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;  
 Cell 74, 597-608, 1993  
 A>Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic  
 A:Reference number: A47537; MUID:93364977; PMID:8356789  
 A:Accession: B47537  
 A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-233 <BOI>  
 A:Cross-references: GB:L20121; NID:g510900; PIDN:CAA80661.1; PID:g510901  
 A:Accession: C47537  
 A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-69, '71-125, 189-233 <BO2>  
 A:Cross-references: GB:L20122; NID:g623236; PIDN:CAA80662.1; PID:g623237  
 C:Genetics:  
 A:Gene: GDB:BCL2L  
 A:Cross-references: GDB:228079  
 C:Superfamily: bcl transforming protein

C:Keywords: alternative splicing; apoptosis  
 F:1-233/Product: apoptosis regulator bcl-xl #status predicted <MA2>  
 F:1-125,189-233/Product: apoptosis regulator bcl-xs #status predicted <MA2>

Query Match 9.1%; Score 135; DB 2; Length 233;  
 Best Local Similarity 21.3%; Pred. No. 7.3e-05;  
 Matches 53; Conservative 38; Mismatches 82; Indels 76; Gaps 10;

QY 84 VVDYFTHIRIRONGMEMF-----GAPGLPCGVQPEHE----- 114  
 ||| : : : : :  
 Db 9 VVDYFTHIRIRONGMEMF-----GAPGLPCGVQPEHE----- 68  
 QY 115 -----MMRVAGTTFEKKHAENFTFCEOLLAVPRISLSLQDVYR 154  
 : : : : :  
 Db 69 TGHSSSLDAREVIMAAVKAQALREAGDEFEELRRRAFSDLSLTHTPGTAQVSFEQYVN 128  
 QY 155 TVGNAQTQCCPMSYGRLLIGLISFGGFVAAKMESV--ELQGVRLNFYVTSLEFKTRIRN 212  
 : : : : :  
 Db 129 -----ELFRDGVNMGRIYAFESFGG---ALCVESVDKEMQVLVSRIAMMATYLVNDHL-E 179  
 QY 213 NMKEHNSMDPMTLGKOMEDEY-ERAEKVGRRKRRMSMGAGVTAGATGIVGVV 271  
 : : : : :  
 Db 180 PWIQEGGWDTFVEL-----YGNNAAESRKQGERFNRWFLG-----MTVAGVYL 225  
 QY 272 CGRRMFSLK 280  
 : : : : :  
 Db 226 LG-SLFSRK 233

## RESULT 4

BCL-X protein - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 02-Mar-2001  
 C:Accession: S51761; S51762  
 R:Michaelidis, T.M.  
 submitted to the EMBL Data Library, November 1994  
 A:Reference number: S51761  
 A:Accession: S51761  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-233 <MIC>  
 A:Cross-references: EMBL:X82537; NID:g607176; PIDN:CAA57886.1; PID:g607177  
 A:Experimental source: embryonic; brain  
 A:Status: S51762  
 A:Accession: S51762  
 A:Molecule type: DNA  
 A:Residues: 1-125,189-233 <MI2>  
 A:Cross-references: EMBL:X82537; NID:g607176; PIDN:CAA57887.1; PID:g607178  
 A:Experimental source: embryonic; brain  
 A:Note: smaller form due to splicing  
 C:Genetics:  
 A:Insertion: 125/3  
 C:Superfamily: bcl transforming protein

Query Match 9.1%; Score 135; DB 2; Length 233;  
 Best Local Similarity 21.3%; Pred. No. 7.3e-05;  
 Matches 53; Conservative 38; Mismatches 82; Indels 76; Gaps 10;

QY 84 VVDYFTHIRIRONGMEMF-----GAPGLPCGVQPEHE----- 114  
 ||| : : : : :  
 Db 9 VVDYFTHIRIRONGMEMF-----GAPGLPCGVQPEHE----- 68  
 QY 115 -----MMRVAGTTFEKKHAENFTFCEOLLAVPRISLSLQDVYR 154  
 : : : : :  
 Db 69 TGHSSSLDAREVIMAAVKAQALREAGDEFEELRRRAFSDLSLTHTPGTAQVSFEQYVN 128  
 QY 155 TVGNAQTQCCPMSYGRLLIGLISFGGFVAAKMESV--ELQGVRLNFYVTSLEFKTRIRN 212  
 : : : : :  
 Db 129 -----ELFRDGVNMGRIYAFESFGG---ALCVESVDKEMQVLVSRIAMMATYLVNDHL-E 179  
 QY 213 NMKEHNSMDPMTLGKOMEDEY-ERAEKVGRRKRRMSMGAGVTAGATGIVGVV 271  
 : : : : :  
 Db 226 LG-SLFSRK 233

Db 180 PWIOENGMDTFVDL-----YGNNAASRKQGERNRNMFLLG-----MTVAGVVL 225  
 QY 272 CGRMFSLK 280  
 Db 226 LG-SLFSRK 233

RESULT 5  
 bcl-x long - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999  
 C:Accession: I49056; S52866  
 R:Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.  
 J. Immunol. 153, 4388-4398, 1994  
 A>Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.  
 A:Reference number: I49055; MUID:95052604; PMID:7963517  
 A:Accession: I49056  
 A>Status: preliminary; translated from GB/EMBL/DDbJ  
 A:Molecule type: mRNA  
 A:Residues: 1-233 <RES>  
 A:Cross-references: EMBL:U0101; NID:9506647; PIDN:AAA82173.1; PID:9506648  
 R:Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.  
 A:Submitted to the EMBL Data Library, November 1994  
 A:Description: IL-5 inhibits anti-IgM-induced apoptosis in an immature B cell line throu  
 A:Reference number: S52866  
 A:Accession: S52866  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-233 <KAM>  
 A:Cross-references: EMBL:X83574; NID:9695622; PIDN:CAA58557.1; PID:9695623  
 C:Superfamily: bcl transforming protein

Query Match 8.9%; Score 132; DB 2; Length 233;  
 Best Local Similarity 20.9%; Pred. No. 0.00014;  
 Matches 52; Conservative 39; Mismatches 82; Indels 76; Gaps 10;

QY 84 VVDYFTHIRIRONGMEWF-----GA 102  
 Db 9 VVDFLSYKLSQKGYSWQSPDVEENKTEAPEETEARETPSALINGNPSMHLADSPAVNGA 68  
 QY 103 PGLPCGVOPEN-----EMMRVMTIFEKKHAENFETFCEDLLAVPRISFLYODVVR 154  
 Db 69 TGHSSSLDAREVLPMAAVKQALREAGDEFELRYRAFSDLTSQLHTPGTAYQSEFQYVN 128  
 QY 155 TVGNAQTDQCPMSYGRLLIGLISFGGFVAAKMESV--ELQGVNRNLFVYTSLFITRI RN 212  
 Db 129 -----ELFRDGVNMGRIYAFESFGG---ALCVESYDKEMQVLVSRIASMMATYINDHL-E 179  
 QY 213 NMEKHNRSMDDEFTLGRKQKMEY-ERAEAEKVGRRKONRRMSMGAGVTAGATGIVGVV 271  
 Db 180 PWIOENGMDTFVDL-----YGNNAASRKQGERNRNMFLLG-----MTVAGVVL 225

QY 272 CGRMFSLK 280  
 Db 226 LG-SLFSRK 233

RESULT 6  
 bcl-x long - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 16-Jul-1999  
 C:Accession: I67431  
 R:Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.  
 Endocrinology 136, 232-241, 1995  
 A>Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equi  
 constitutive bcl-2 and bcl-x long messenger ribonucleic acid levels.  
 A:Reference number: I53295; MUID:95129487; PMID:7828536  
 A:Accession: I67431  
 A>Status: preliminary; translated from GB/EMBL/DDbJ  
 A:Molecule type: mRNA  
 A:Residues: 1-233 <RES>

A:Cross-references: EMBL:U34963; NID:q1004376; PIDN:AAA7686.1; PID:q1004377  
 C:Superfamily: bcl transforming protein

Query Match 8.5%; Score 126; DB 2; Length 233;  
 Best Local Similarity 21.6%; Pred. No. 0.0005;  
 Matches 54; Conservative 36; Mismatches 82; Indels 78; Gaps 11;

QY 84 VVDYFTHIRIRONGMEWF-----GAPGLPCGVOPEN----- 114  
 Db 9 VVDFLSYKLSQKGYSWQSPDVEENKTEAPEETEARETPSALINGNPSMHLADSPAVNGA 68  
 QY 115 -----MMRVMTIFEKKHAENFETFCEDLLAVPRISFLYODVVR 154  
 Db 69 TGHSSSLDAREVLPMAAVKQALREAGDEFELRYRAFSDLTSQLHTPGTAYQSEFQYVN 128  
 QY 155 TVGNAQTDQCPMSYGRLLIGLISFGGFVAAKMESV--ELQGVNRNLFVYTSLFITRI RN 212  
 Db 129 -----ELFRDGVNMGRIYAFESFGG---ALCVESYDKEMQVLVSRIASMMATYINDHL-E 179  
 QY 213 NMEKHNRSMDDEFTLGRKQKMEY-ERAEAEKVGRRKONRRMSMGAGVTAGATGIVGVV 270  
 Db 180 PWIOENGMDTFVDL-----YGNNAASRKQGERNRNMFLLG-----MTVAGVVL 224  
 QY 271 CGRMFSLK 280  
 Db 225 LG-SLFSRK 233

RESULT 7  
 A37332  
 transforming protein (bcl-2-alpha) - chicken  
 C:Species: Gallus gallus (chicken)  
 C>Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 23-Feb-1997  
 C:Accession: A37332; S35453  
 R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.  
 Nucleic Acids Res. 20, 4187-4192, 1992  
 A>Title: Isolation and characterization of the chicken bcl-2 gene: expression in a va  
 A:Reference number: A37332; MUID:92375724; PMID:1508712  
 A:Accession: A37332  
 A>Status: nucleic acid sequence not shown  
 A:Molecule type: DNA  
 A:Residues: 1-233 <EGU>  
 A:Cross-references: EMBL:D11381  
 C:Genetics:  
 A:Introns: 189/3  
 C:Superfamily: bcl transforming protein; transmembrane protein  
 C:Keywords: mitochondrion; transforming protein; transforming protein

Query Match 7.8%; Score 116; DB 2; Length 233;  
 Best Local Similarity 19.9%; Pred. No. 0.0042;  
 Matches 48; Conservative 38; Mismatches 77; Indels 78; Gaps 11;

QY 79 DIEGFVVDYFTHIRIRONGMEWF-----APGLPC----- 107  
 Db 10 DNREIVLKYTHYKLSQKGYDWAAGEDRPVPAPAPAAVAAGASHHRRPEPGSA 69  
 QY 108 -----GVOPN-----HEMMRVMTIFEKKHAENFETFCEDLLAVPRISFLYODVVR 154  
 Db 70 AASEVPAEGLRPAAPGVHIALRQAGDEFERRRQORDAQMGSGLHLTP---FTHAGFVA 126  
 QY 155 TVGNAQTDQCPMSYGRLLIGLISFGGFVAAKMESV--ELQGVNRNLFVYTSLFITRI RN 212  
 Db 127 VVEELFRD--GVNMGRIYAFEFEGVAC---VESVNRKMSPLDNTATWMTETVLRNHL-H 180  
 QY 213 NMEKHNRSMDDEFTLGRKQKMEY-ERAEAEKVGRRKONRRM-----SMIGAGVTAG 262  
 Db 181 NWIDNGWDAFVELYGSMPKLPDFS-----WISLKITLSLVIVGACITITG 227  
 QY 263 A 263  
 Db 228 A 228

## RESULT 8

TVHDA1

transforming protein bcl-2, splice form alpha - human

C:Species: Homo sapiens (man)

C&gt;Date: 31-Dec-1988 #sequence\_revision 07-Jun-1996 #text\_change 15-Oct-1999

C:Accession: G37332; A29409; S02452; A24428; A27622; B27622

R:Enguchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety

A:Reference number: A37332; MUID:92375724; PMID:1508712

A:Accession: C37332

A:Status: nucleic acid sequence not shown: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-239 &lt;EGU&gt;

A&gt;Note: this report is a correction

R:Tsujimoto, Y.; Croce, C.M.

Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986

A:Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene

A:Reference number: A29409; MUID:86259760; PMID:3523487

A:Accession: A29409

A:Molecule type: mRNA

A:Residues: 1-95, 'A', 'G', '111-236, 'S', '238-239 &lt;TSD&gt;

A:Cross-references: GB:M13944; NID:q179366; PIDN:AAA51813.1; PID:q179367

A&gt;Note: this sequence has been corrected in reference A37332

R:Seio, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett, S.; Goldman, P.; Korsmeyer

EMBO J. 7, 123-131, 1988

A:Title: Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2

A:Reference number: S02452; MUID:88196071; PMID:2834197

A:Accession: S02452

A:Molecule type: mRNA

A:Residues: 1-239 &lt;SET&gt;

R:Cleary, M.L.; Smith, S.D.; Sklar, J.

Cell 47, 19-28, 1986

A:Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin

A:Reference number: A24428; MUID:87002488; PMID:2875799

A:Accession: A24428

A:Molecule type: mRNA

A:Residues: 1-58, 'T', '60-116, 'R', '118-239 &lt;CUE&gt;

A:Cross-references: GB:M14745; NID:q179370; PIDN:AAA5591.1; PID:q179371

R:Ha, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakshi, A.

Oncogene Res. 2, 263-275, 1988

A:Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphoma:

A:Reference number: A27622; MUID:88217344; PMID:3285301

A:Accession: A27622

A:Molecule type: mRNA

A:Residues: 1-58, 'T', '60-239 &lt;HUA&gt;

A:Accession: B27622

A:Molecule type: DNA

A&gt;Note: the sequence was determined from the germline gene

C:Comment: Constitutive expression of Bcl2 following t(14;18) chromosomal translocation

C:Genetics:

A:Gene: GDB:BCL2

A:Cross-references: GDB:119031; OMIM:151430

A:Map position: 18q21.3-18q21.3

C:Function:

A:Description: blocks apoptosis in hematopoietic cells

C:Superfamily: bcl transforming protein

C:Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; proto

Query Match 7.8%; Score 116; DB 1; Length 239;

Best Local Similarity 19.4%; Pred. No. 0.0043;

Matches 48; Conservative 39; Mismatches 76; Indels 84; Gaps 10;

QY 79 DIEGFVVDFTFTRIRONGMEW----- 100

DB 10 DNEELVMTKIHYKLSQRYEMDAGVGAAPAPAPGIFSSQPGHTPPAASRDEAVAT 69

QY 101 -----GAPGLPGC-----VQP-EHEMRYMGTIFEKKAENFEFCEDLLAVPRISFSL 148

DB 70 SPLQTPAAGGAAGPALSPVPVYVHLTRQAGDDFSRRYRDRFAEMSSQLHLTPFARGR 129

QY 149 YQDVVATVGNATQDCPMYSGRLIGLISGCGVAAKMMESV--ELQGOVRNLFVYTSLEFI 206

P 1 1

DB 130 FATVVE-----ELFRGVMMGRIVAFEEFGVVC---VESVREKMSPLVDNALMWTEYL 181

QY 207 KTRIRNNWKEHNSWDFTLT-GKQKEDERYEAERKVRKRNKRW-----SMIG 256

DB 182 NRRL-HTWIODNGMDAFVLYGPSRPLFDPS-----WLSLKTLLSLALVG 227

QY 257 AGVTAQA 263

DB 228 ACITLGA 234

## RESULT 9

TVMSA1

transforming protein bcl-2-alpha - mouse

C:Species: Mus musculus (house mouse)

C&gt;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 18-Jun-1999

C:Accession: A25960; E37332

R:Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.

Cell 49, 455-463, 1987

A:Title: Molecular analysis of mbcl-2: structure and expression of the murine gene ho

A:Reference number: A50893; MUID:87187643; PMID:3032455

A:Accession: A25960

A:Molecule type: DNA

A:Residues: 1-236 &lt;NEG&gt;

A:Cross-references: GB:I31532; GB:M16506; NID:q468336; PIDN:AAA37282.1; PID:q387109

R:Enguchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a va

A:Reference number: A37332; MUID:92375724; PMID:1508712

A:Accession: E37332

A:Status: preliminary; nucleic acid sequence not shown: not compared with conceptual

A:Molecule type: DNA

A:Residues: 1-33, 'E', '34-220, 'AL', '223-236 &lt;EGU&gt;

C:Genetics:

A:Gene: BCL2

A:introns: 192/3

C:Superfamily: bcl transforming protein

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane

Query Match 7.7%; Score 113.5; DB 1; Length 236;

Best Local Similarity 20.0%; Pred. No. 0.0073;

Matches 49; Conservative 38; Mismatches 75; Indels 83; Gaps 11;

QY 79 DIEGFVVDFTFTRIRONGMEW-----FGA---PGLPGVQPE----- 112

DB 10 DNEELVMTKIHYKLSQRYEMDAGDADAAPGAPTPGI-FSPQESNPMFVAREMAAR 68

QY 113 -----HEMRYMGTIFEKKAENFEFCEDLLAVPRISFSLYQ 150

DB 69 TSPLRPLVATAGPALSPVPCVHLTRRAGDDFSRRYRDRFAEMSSQLHLTPFARGRFA 128

QY 151 DYVRYVGNATQDCPMYSGRLIGLISGCGVAAKMMESV--ELQGOVRNLFVYTSLEFIKT 208

DB 129 TVVE-----ELFRDGVNNGRIYAFEEFGVVC---VESVREKMSPLVDNALMWTEYLNR 180

QY 209 RIRNNWKEHNSWDFTLT-GKQKEDERYEAERKVRKRNKRW-----SMIGAG 258

DB 181 HL-HTWIODNGMDAFVLYGPSRPLFDPS-----WLSLKTLLSLPWWGAC 226

QY 259 VTAGA 263

DB 227 ITLGA 231

RESULT 10

BCL-2 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C&gt;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 16-Jul-1999

C:Accession: I67442

R:Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.

Endocrinology 136, 232-241, 1995



A:Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equivalent expression of bcl-2 and bcl-xl in granulosa cells and constitutive bcl-2 and bcl-xl in theca cells.  
A:Reference number: 153295; PMID:95129487; PMID:7828536  
A:Accession: 167432  
A:Status: preliminary; translated from GR/EMBL/DBD  
A:Molecule type: mRNA  
A:Residues: 1-236 <RES>  
A:Cross-references: EMBL:U03966; MID:g1004378; PIDN:AAA77687.1; PID:g1004379  
C:Superfamily: bcl transforming protein

Db	69	TSPLRPVANNAPALSPVPVPHVHLLTTLRRADDSESRRRRDFEAEMSQLHILTEPTARGRA	128
QY	151	DYATVTVGAQIQDQCPMSYGRLLIGLISRGVAAKMMESVLEQOVRLLFVYTSLEFKTRI	210
Db	129	TVVE-----ELFRDGVMMGRVAFEEFGVWCVGSVNR-EMSLPYDIALMTMEYLNRLH	182
QY	211	RNNKKEHNRSDDEMTL-GROMKEDYERAAEKVGRKKORRW-----SMIGAVY	260
Db	183	HTWIONGCGWDAAVEVLEGPSMRPLPDFS-----WLSTKTLTLATLVGACIT	228
QY	261	AGA 263	
Db	229	LGA 231	

RESULT 14  
I49057  
bcl-x transmembrane deleted - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999  
C:Accession: I49057  
R:Feng, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.  
J. Immunol. 153, 4388-4398, 1994  
A:Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes  
A:Reference number: I49055; MUID:95052604; PMID:7963517  
A:Accession: I49057  
A:Status: preliminary; translated from GB/EWBL/DDbJ  
A:Molecule type: mRNA  
A:Residues: 1-214 <RES>  
A:Cross-references: EMBL:U01002; NID:g506649; PIDN:AA82174.1; PID:g506650  
C:Genetics:  
A:Gene: bcl-x-long  
A:Superfamily: bcl transforming protein

Query Match	7.3%;	Score 108;	DB 2;	Length 214;
Best Local Similarity	19.2%;	Pred. No. 0.021;		
Matches	37;	Conservative	31;	Mismatches 65; Indels 60; Gaps 6;

  

QY	84	VVDYFTHIRIRONGMEWF-----	GA	102
		: : : : :		
Db	9	VDFLSLTSLQSKGVSWSQFSDVEENRTARETEERETPSA1INGNPWHLNDSPAVNGA		68
		: : : : :		
QY	103	PGLEQGVQPEH-----EMKRVNGTITPEKKHAENETFEFCOLLAVPRLISLVQDVYR		154
		: : : : :		
Db	69	TGHSSTLAREYIIPAAVAKQALREAGDEFELLYRRAFSDLTSQLHTTPETAQAQSEFQVNA		128
		: : : : :		
QY	155	TVGNAQTQDCPMYSYGRITGLISFGGFAVAKMMEYS--ELQGVNRILFVYTSLFIKTRIRN		212
		: : : : :		
Db	129	-----ELPRDQGVNGRIVAFESFGG--ALCVESYDKEMQVLVSRLASMATYINDLH-L		179
		: : : : :		
QY	213	NWKEHNRSLQDQEM		225
		: : : : :		
Db	180	PMIDQENGGMDFTFV		192
		: : : : :		

RESULT 15  
AE1901  
WD:Repeat containing protein [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp.  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002  
C:Accession: AE1901  
Nakaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchishima, N.; Shimpō, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena* sp. strain PCC 7120  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AE1901  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1328 <KUR>  
A:Cross-references: GB:BA000019; PIDN:BAE72716.1; PID:917130104; GSPDB:GN00179

A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: al10759

Query Match	7.3%	Score 108	DB 2	Length 1329
Best Local Similarity	22.7%	Pred. No. 0.23		
Matches 68	Conservative 39	Mismatches 101	Indels 92	Gaps 14

[illegible]

```
Search completed: February 24, 2003, 11:55:06
Job time : 20 secs
```

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 24, 2003, 11:51:39 ; Search time 11 seconds  
(without alignments)  
1055.761 Million cell updates/sec

Title: US-09-993-420A-3

Perfect score: 1479  
Sequence: 1 MTRCRADNLSLTNPAYRRRTM.....AGAGTGVVCGRMFLSK 280

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1479	100.0	280	1	CEB9_CAEEL
2	898.5	60.8	271	1	CEB9_CAEEL
3	151	10.2	193	1	BCLW_MOUSE
4	150	10.1	193	1	BCLW_MOUSE
5	135	9.1	233	1	BCLX_HUMAN
6	135	9.1	233	1	BCLX_HUMAN
7	132	8.9	233	1	BCLX_MOUSE
8	131	8.9	233	1	BCLX_MOUSE
9	125.5	8.5	228	1	AR1_XENLA
10	118.5	8.0	229	1	BCL2_BOVIN
11	118	7.8	233	1	BCL2_CHICK
12	116	7.8	233	1	BCL2_CHICK
13	116	7.8	233	1	BCL2_HUMAN
14	114.5	7.7	229	1	BCL2_HUMAN
15	113.5	7.6	229	1	BCL2_HUMAN
16	112	7.6	177	1	BCL2_HUMAN
17	110.5	7.5	236	1	BCL2_HUMAN
18	95	6.4	350	1	BCL2_HUMAN
19	90	6.1	274	1	YOHM_ECOLI
20	89.5	6.1	1217	1	YHCR_BACST
21	88	5.9	436	1	YHCR_BACST
22	87	5.9	347	1	YHCR_BACST
23	86.5	5.8	358	1	YHCR_BACST
24	85	5.7	347	1	YHCR_BACST
25	84	5.7	347	1	YHCR_BACST
26	84	5.6	361	1	YHCR_BACST
27	83	5.6	516	1	YHCR_BACST
28	83	5.6	545	1	YHCR_BACST
29	82.5	5.6	574	1	YHCR_BACST
30	82.5	5.6	852	1	YHCR_BACST
31	82	5.5	845	1	YHCR_BACST
32	81.5	5.5	418	1	YHCR_BACST
33	81.5	5.5	518	1	YHCR_BACST

34	81.5	5.5	661	1	DYN_DROME	Q2426 drosophila
35	81	5.5	391	1	Y532_METJA	Q5752 methanococ
36	81	5.5	515	1	NIED_BRAJA	P06121 bradyrhizob
37	81	5.5	528	1	ATPB_BOVIN	P00829 bos taurus
38	80	5.4	491	1	NIED_AZOVI	P07328 azotobacter
39	80	5.4	529	1	ATPB_HUMAN	P06376 homo sapien
40	79.5	5.4	372	1	HEXB_HAEIN	P44326 h riboflavi
41	79.5	5.4	649	1	HEXB_STREN	P14160 streptococc
42	79.5	5.4	971	1	PGH2_BORBU	O51246 borrelia bu
43	79	5.3	604	1	PGH2_BORBU	P35355 rattus norv
44	79	5.3	631	1	THIC_SALTY	Q91917 salmoneilla
45	79	5.3	639	1	BACQ_BACIL	O68008 b bacitraci

## ALIGNMENTS

RESULT 1  
ID CEB9\_CAEEL STANDARD: PRT; 280 AA.  
AC P41958:  
DT 01-NOV-1995 (rel. 32, Created)  
DT 01-NOV-1995 (rel. 32, Last sequence update)  
DT 15-JUN-2002 (rel. 41, Last annotation update)  
DE Apoptosis regulator ced-9 (Cell death protein 9).  
GN CED-9 OR P07C4.8.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
OC Rhabditidae; Pelodierinae; Caenorhabditis.  
OX NCBI\_TaxId=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Bristol N2;  
RX MEDLINE=94170367; PubMed=7907274;  
RA Hengartner M.O., Horvitz H.R.;  
RT "C. elegans cell survival gene ced-9 encodes a functional homolog of  
RL the mammalian proto-oncogene bcl-2.";  
RL Cell 76:665-676(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Bristol N2;  
RX Berks M., Durbin R.;  
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP CHARACTERIZATION, AND MUTAGENESIS.  
RC STRAIN-Bristol N2;  
RX MEDLINE=97177114; PubMed=9024666;  
RA Specter M.S., Desnoyers S., Hoepfner D.J., Hengartner M.O.;  
RT "Interaction between the C. elegans cell-death regulators CED-9 and  
RL CED-4.";  
RL Nature 385:653-656(1997).  
CC -I- FUNCTION: CAN BOTH PROMOTE AND PREVENT PROGRAMMED CELL DEATH  
CC (APOPTOSIS) WHICH IS ESSENTIAL FOR DEVELOPMENT AND HOMEOSTASIS. IT  
CC DOES THIS BY ANTAGONIZING THE DEATH PROMOTING/PREVENTING  
CC ACTIVITIES OF CED-3, CED-4S AND CED-4L. IT BINDS STRONGLY TO CED-  
CC 4S AND LESS SO TO CED-4L.  
CC -I- DEVELOPMENTAL STAGE: ABUNDANT EXPRESSION IS SEEN IN THE EMBRYOS  
CC AND THE ADULTS.  
CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
CC -I- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
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CC or send an email to [license@isb-sdb.ch](mailto:license@isb-sdb.ch)).  
CC -----  
CC EMBL: L26545; AAA20080.1; -  
CC EMBL: Z29443; CAA82573.2; -  
CC DR

DR WormPep; T07C4.8; CE00599.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH4.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; FALSE\_NEG.  
 DR PROSITE: PS01258; BH2; FALSE\_NEG.  
 DR PROSITE: PS01260; BH4\_1; FALSE\_NEG.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 DR Apoptosis.  
 KW Apoptosis.  
 FT DOMAIN 80 99 BH4.  
 FT DOMAIN 160 179 BH1.  
 FT DOMAIN 213 229 BH2.  
 FT MUTAGEN 149 149 Y->N: IN N1653; LETHAL PHENOTYPE.  
 FT MUTAGEN 169 169 G->E: IN G169E; GAIN OF FUNCTION.  
 SQ SEQUENCE 280 AA; 31824 MW; 7603675E490DD3EB CRC64;

Query Match 100.0%; Score 1479; DB 1; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 1,4e-126;  
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTRCTADNSTLTNPAYRRRTMATGEMKEFLGKTEPTFGINSADADLPSPROASTRRM 60  
 DB 1 MTRCTADNSTLTNPAYRRRTMATGEMKEFLGKTEPTFGINSADADLPSPROASTRRM 60  
 OY 61 SIGESIDGKINDMEEPRLDIEGFVVDYFTHIRIRONGEMFGAGLPGVQPEHEMMRWG 120  
 DB 61 SIGESIDGKINDMEEPRLDIEGFVVDYFTHIRIRONGEMFGAGLPGVQPEHEMMRWG 120  
 OY 121 TIEFKKAENFEETCEQLLAVPRISFSLYODVYRTVGNQATDQCPMSYRLGLISFGGF 180  
 DB 121 TIEFKKAENFEETCEQLLAVPRISFSLYODVYRTVGNQATDQCPMSYRLGLISFGGF 180  
 OY 181 VAAKMMESVLOGOVNLFYVTSLFITKTRIRNNKKEHNSWDDEFTMLGKMKEDYERABA 240  
 DB 181 VAAKMMESVLOGOVNLFYVTSLFITKTRIRNNKKEHNSWDDEFTMLGKMKEDYERABA 240  
 OY 241 EKYGRKRRNRMSMIGAGVTAGATGIVGVVCGRMFSLK 280  
 DB 241 EKYGRKRRNRMSMIGAGVTAGATGIVGVVCGRMFSLK 280

RESULT 2  
 CED9\_CAEBR  
 ID CED9\_CAEBR STANDARD; PRT: 271 AA.  
 AC P41957;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator ced-9 (Cell death protein 9).  
 GN CED-9.  
 OS Caenorhabditis briggsae.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoides;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 ON NCBI\_TaxID=6238;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94170367; PubMed=7907274;  
 RA Hengartner M.O., Horvitz H.R.;  
 RT "C. elegans cell survival gene ced-9 encodes a functional homolog of  
 RT the mammalian proto-oncogene bcl-2.";  
 RL Cell 76:665-676(1994).  
 CC -1- FUNCTION: PROTECT CELLS THAT NORMALLY SURVIVE FROM UNDERGOING  
 CC PROGRAMMED CELL DEATH (APOPTOSIS) WHICH IS ESSENTIAL FOR  
 CC DEVELOPMENT AND HOMEOSTASIS.  
 CC -1- DEVELOPMENTAL STAGE: ABUNDANT EXPRESSION IS SEEN IN THE EMBRYOS  
 CC AND THE ADULTS.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: L26546; AAA20077.1;  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH4.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; FALSE\_NEG.  
 DR PROSITE: PS01258; BH2; FALSE\_NEG.  
 DR PROSITE: PS01260; BH4\_1; FALSE\_NEG.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 DR Apoptosis.  
 KW Apoptosis.  
 FT DOMAIN 80 99 BH4.  
 FT DOMAIN 159 179 BH1.  
 FT DOMAIN 213 228 BH2.  
 SQ SEQUENCE 271 AA; 31214 MW; CDC135B0C539201F CRC64;

Query Match 60.8%; Score 898.5; DB 1; Length 271;  
 Best Local Similarity 65.0%; Pred. No. 4.7e-74;  
 Matches 178; Conservative 34; Mismatches 45; Indels 17; Gaps 6;

OY 8 NSLTPTARRRTMATGEMKEFLGKTEPTFGINSADADLP-SPSROASTRRMSSTESTI 66  
 DB 14 NSSQN-TFRRTMATSEMERELSTKDAEPNFGM----QRTSPSTPTSTPTRRMSIDST 68  
 OY 67 DGIKINDMEEPRLDIEGFVVDYFTHIRIRONGEMFGAGLPGVQPEHEMMRWGVTIEKK 126  
 DB 69 --RIYDMEEPRLDIEGFVVDYFTHIRIRONGEMFGAGLPGVQPEHEMMRWGVTIEKK 126  
 OY 127 HAENFEETCEQLLAVPRISFSLYODVYRTVGNQATDQCPMSYRLGLISFGFVAAKM 186  
 DB 127 HMEMEFNSEQLLAVPRISFSLYODVYRTVGNQATDQCPMSYRLGLISFGFVAAKM 186  
 OY 187 ESVELOGOVNLFYVTSLFITKTRIRNNKKEHNSWDDEFTMLGKMKEDYERAEKYGRR 246  
 DB 187 ESAELOGOVNLFYVTSLFITKTRIRNNKKEHNSWDDEFTMLGKMKEDYERAEKYGRR 246  
 OY 247 KÖNRMSWIGAGVTAGATGIVGVVCGRMFSLK 280  
 DB 247 LKS--WSTIGASV-----IATVCGRLIFSPK 271

RESULT 3  
 BCLW\_MOUSE  
 ID BCLW\_MOUSE STANDARD; PRT: 193 AA.  
 AC P70345;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-W.  
 GN BCL2L2 OR BCLW.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96358615; PubMed=8761287;  
 RA Gibson J., Holmgren S.P., Huang D.C., Bernard O., Copeland N.G.,  
 RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;

"bcl-w, a novel member of the bcl-2 family, promotes cell survival."; Oncogene 13:665-675(1996).

[2]

SEQUENCE FROM N.A.

RC STRAIN=C57BL/10J;

RX MEDLINE=98160183; PubMed=9500547;

RA Ross A.J., Maynair K.G., Moss J.E., Parlow A.F., Skinner M.K., Russell L.D., Macgregor G.R., "Testicular degeneration in bclw-deficient mice."; Nat. Genet. 18:251-256(1998).

RL Nat. Genet. 18:251-256(1998).

CC -1- FUNCTION: PROMOTES CELL SURVIVAL.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON, AND SALIVARY GLAND.

CC -1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC FUNCTION.

CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.

CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

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DR EMBL: U59746; AAB09056.1; -

DR EMBL: AF030769; AAB86430.1; -

DR HSSP: Q07817; IMAZ.

DR MGD: MGI:108052; BCL2L2.

DR InterPro: IPR002475; BCL2\_family.

DR InterPro: IPR000712; BCL2\_BH.

DR InterPro: IPR003093; BCL2\_BH4.

DR Pfam: PF00452; BCL-2; 1.

DR Pfam: PF02180; BH4; 1.

DR SMART: SM00337; BCL; 1.

DR SMART: SM00265; BH4; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR PROSITE: PS01080; BH1; 1.

DR PROSITE: PS01258; BH2; 1.

DR PROSITE: PS01260; BH4\_1; 1.

DR PROSITE: PS50063; BH4\_2; 1.

DR Apoptosis.

KW Apoptosis.

FT DOMAIN 9 29 BH4.

FT DOMAIN 85 104 BH1.

FT DOMAIN 136 151 BH2.

SQ SEQUENCE 193 AA; 20790 MW; 36CA185F5945DFB4 CRC64;

Query Match 10.2%; Score 151; DB 1; length 193;

Best Local Similarity 24.3%; Pred. No. 1.4e-06;

Matches 51; Conservative 31; Mismatches 92; Indels 36; Gaps 8;

RESULT 4

BCIM\_HUMAN STANDARD; PRT; 193 AA.

ID BCL2\_HUMAN

AC 092843;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DE 15-JUN-2002 (Rel. 41, Last annotation update)

DE Apoptosis regulator Bcl-w.

GN BCL2L2 OR BCLW OR KIA0271.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_Taxid=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96358615; PubMed=8761287;

RA Gibson L., Holmgren S.P., Huang D.C., Bernard O., Copeland N.G., Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.; "bcl-w, a novel member of the bcl-2 family, promotes cell survival."; Oncogene 13:665-675(1996).

RL [2]

RN SEQUENCE FROM N.A.

RP TISSUE=Brain;

RX MEDLINE=97191544; PubMed=9039502;

RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayashi Y., Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.; "Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (KIA0201-KIA0280) deduced by analysis of cDNA clones from cell line K6-1 and brain."; DNA Res. 3:321-329(1996).

RL DNA Res. 3:321-329(1996).

CC -1- FUNCTION: PROMOTES CELL SURVIVAL.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON, AND SALIVARY GLAND.

CC -1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC FUNCTION.

CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.

CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

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-----

DR EMBL: U59747; AAB09055.1; -

DR EMBL: D87461; BAA19666.1; -

DR HSSP: Q07817; IMAZ.

DR Genew: HGNC:995; BCL2L2.

DR MIM: 601931; -

DR InterPro: IPR002475; BCL2\_family.

DR InterPro: IPR000712; BCL2\_BH.

DR InterPro: IPR003093; BCL2\_BH4.

DR Pfam: PF00452; BCL-2; 1.

DR Pfam: PF02180; BH4; 1.

DR SMART: SM00337; BCL; 1.

DR SMART: SM00265; BH4; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR PROSITE: PS01080; BH1; 1.

DR PROSITE: PS01258; BH2; 1.

DR PROSITE: PS01260; BH4\_1; 1.

DR PROSITE: PS50063; BH4\_2; 1.

DR Apoptosis.

KW Apoptosis.

FT DOMAIN 9 29 BH4.

FT DOMAIN 85 104 BH1.

FT DOMAIN 136 151 BH2.

SQ SEQUENCE 193 AA; 20774 MW; 3792243A50281761 CRC64;

Query Match 10.1%; Score 150; DB 1; Length 193;  
 Best Local Similarity 24.3%; Pred. No. 1,7e-06;  
 Matches 51; Conservative 30; Mismatches 93; Indels 36; Gaps 8;

Y 79 DIEGFVYDFTFRIRONCEMEFAPGLPCGVQPEHEMRKVGITFEKKHAENFEFCEQL 138  
 B 9 DTRALVADFEVYKLRKQKGYCGAGPAGPADPLHOAMRAAGDEFEFRFRTEFSDLAQL 68  
 Y 139 LAVP-----RISFSLYODVFTVGNMAQDQPMISYGRLLIGISFCFVAAKMM--ES 168  
 B 69 HTVFGSMAQRTQVSDLEFPG-----GPMGRVIAFFVFGALCAESVKKEM 115  
 Y 189 VELQGVARNLFVYTSLEFKTRIRNNKEMHNSMDEMTLIGKOMEDEYERAEKVRKKQ 248  
 B 116 EPLVGOVQEWNV---AYLEFRLA-DWIHSSGMAEFAL-----YGDGALLE-ARRLR 163  
 Y 249 NRWMSMGAGVTAGAIGVGVYVGRMMFS 278  
 B 164 EGNMAYVRT-VLTGVALGALVTVGAFFAS 192

RESULT 5  
 BCLX HUMAN STANDARD; PRT; 233 AA.

AC 007817; 092976;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-x.  
 GN BCL2L1 OR BCL2L OR BCLX.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).  
 RX MEDLINE=93364977; PubMed=8358789;  
 RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,  
 RA Turka L.A., Mao X., Nunez G., Thompson C.B.;  
 RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator  
 of apoptotic cell death.";  
 RL Cell 74:597-608(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM BETA).  
 RA Inohara N., Onca S.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP MUTAGENESIS OF GLY-138, AND HETERODIMERIZATION.  
 RX MEDLINE=95372373; PubMed=7644501;  
 RA Sedlak T.W., Oltvai Z.N., Yang E., Wang K., Boise L.H., Thompson C.B.,  
 RA Korsmeyer S.J.;  
 RT "Multiple Bcl-2 family members demonstrate selective dimerizations  
 with Bax.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:7834-7838(1995).  
 RN [4]  
 RP MUTAGENESIS OF BHL AND BH2 DOMAINS.  
 RX MEDLINE=96170038; PubMed=859636;  
 RA Cheng E.H.-Y., Levine B., Boise L.H., Thompson C.B., Hardwick J.M.,  
 RA Korsmeyer S.J.;  
 RT "Bax-independent inhibition of apoptosis by Bcl-XL.";  
 RL Nature 379:554-556(1996).  
 RN [5]  
 RP STRUCTURE BY NMR OF 1-209.  
 RX MEDLINE=97172562; PubMed=9020082;  
 RA Sattler M., Liang H., Nettlesheim D., Meadows R.P., Harlan J.E.,  
 RA Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,  
 RA Thompson C.B., Fesik S.W.;  
 RT "Structure of Bcl-XL-Bax peptide complex: recognition between  
 regulators of apoptosis.";  
 RL Science 275:983-986(1997).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND STRUCTURE BY NMR OF 1-209.  
 RX MEDLINE=96256675; PubMed=8692274;

RA Muchmore S.W., Sattler M., Liang H., Meadows R.P., Harlan J.E.,  
 RA Yoon H.S., Nettlesheim D., Chang B.S., Thompson C.B., Wong S.L.,  
 RA Ng S.L., Fesik S.W.;  
 RT "X-ray and NMR structure of human Bcl-XL, an inhibitor of programmed  
 RT cell death.";  
 RL Nature 381:335-341(1996).  
 RN [7]  
 RP CLEAVAGE BY CASPASES, AND MUTAGENESIS OF ASP-61.  
 RX MEDLINE=98118550; PubMed=9435230;  
 RA Clem R.J., Cheng E.H.-Y., Karp C.L., Kirsch D.G., Ueno K.,  
 RA Takahashi A., Kastan M.B., Griffin D.E., Earnshaw W.C., Velluona M.A.,  
 RA Hardwick J.M.;  
 RT "Modulation of cell death by Bcl-XL through caspase interaction.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:554-559(1998).  
 CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of  
 CC caspases (By similarity). Appears to regulate cell death by  
 CC blocking the voltage-dependent anion channel (VDAC) by binding  
 CC to it and preventing the release of the caspase activator,  
 CC cytochrome c, from the mitochondrial membrane. The Bcl-x(s)  
 CC isoform promotes apoptosis.  
 CC -1- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2.  
 CC heterodimerization with BAX does not seem to be required for anti-  
 CC apoptotic activity.  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR  
 CC ENVELOPE (BY SIMILARITY).  
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: BCL-X(L) (SHOWN HERE), BCL-X(S)  
 CC AND BCL-X(BETA). ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS  
 CC THAT UNDERGO A HIGH RATE OF TURNOVER, SUCH AS DEVELOPING  
 CC LYMPHOCYTES. IN CONTRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING  
 CC LONG-LIVED POSTMITOTIC CELLS, SUCH AS ADULT BRAIN.  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.  
 CC The BH1 and BH2 domains are required for both heterodimerization  
 CC with other Bcl2 family members and for repression of cell death.  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The  
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic  
 CC activity.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; Z23116; CAAB0662.1; -;  
 DR EMBL; Z23115; CAAB0661.1; -;  
 DR EMBL; U72398; AAB17354.1; -;  
 DR PDB; 1BXL; 29-OCT-97.  
 DR PDB; 1LXL; 21-APR-97.  
 DR PDB; 1MAZ; 21-APR-97.  
 DR Genew; HGNC:992; BCL2L1.  
 DR MIM; 600039; -;  
 DR InterPro; IPR002475; BCL2\_family.  
 DR InterPro; IPR000712; BCL2\_BH.  
 DR InterPro; IPR003093; BCL2\_BH4.  
 DR InterPro; IPR004725; BCL2\_reg.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR Pfam; PF02180; BH4; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR SMART; SM00265; BH4; 1.  
 DR TIGRFS; TIGR00865; bcl-2; 1.  
 DR PROSITE; PSS0062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 DR PROSITE; PS01260; BH4; 1.  
 DR PROSITE; PS01260; BH4\_1; 1.









FT DOMAIN 86 100 BH3.  
 FT DOMAIN 129 148 BH1.  
 FT DOMAIN 180 195 BH2.  
 FT TRANSMEM 210 226 POTENTIAL.  
 SQ SEQUENCE 233 AA; 26061 MW; 18BF6FA0441912B2 CRC64;

Query Match 8.9%; Score 131; DB 1; Length 233;  
 Best Local Similarity 20.9%; Pred. No. 0.00011;  
 Matches 52; Conservative 39; Mismatches 82; Indels 76; Gaps 10;

QY 84 VVDYFTHRIKRGKMEWF-----GAPGLPCGVOPHE----- 114  
 DB 9 VVDYFTHRIKRGKMEWF-----GAPGLPCGVOPHE----- 114  
 QY 115 -----NMKVGITFEKKHAENFEFCQGLAVPRISFYQDVVR 154  
 DB 69 TGHSSSLDAREVYIPMAAVYQALREAGDEFLRYRAFSDLISQHLITFGTAVQSEGYLN 128  
 QY 155 TVGNMOTQCPMSYGRLLIGLISFGFVAAKMMESV--ELQGVNRLFYVTSLFIKTRIRN 212  
 DB 129 -----ELFPDGVNMGRIYAFVFEFG--ALCVESYDKEMOVLVSRIATWMTYINDHL-E 179  
 QY 213 NMKEHNRSDPMTLGKQMKEDY-ERAEAEKVRKRRKRRMSMGAGVTAGAIQVGVV 271  
 DB 180 PWIQNGMGMDFFVEL-----YGNMAAESEKRGGERNNRFLTG-----MTLAGVVL 225  
 QY 272 CGRMFSLK 280  
 DB 226 LG-SLEFSRK 233

## RESULT 9

ARL\_XENLA  
 ID ARL\_XENLA STANDARD; PRT: 228 AA.

AC Q91827;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator R1 (XRL) (Fragment).  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 OC Xenopodidae; Xenopus.  
 NX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Head;  
 RX MEDLINE=95331613; PubMed=7607538;  
 RA Cruz-Reyes J., Tata J.R.;  
 RT "Cloning, characterization and expression of two Xenopus bcl-2-like  
 cell survival genes";  
 RL Gene 158:171-179(1995).  
 CC -1- FUNCTION: COULD BE THE HOMOLOG OF MAMMALIAN BCL-W.  
 CC -1- SUBCELLULAR LOCATION: Membrane-bound (Potential).  
 CC -1- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE  
 CC BRAIN OF MID-METAMORPHOSIS TO POST-METAMORPHOSIS TADPOLES AND  
 CC ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
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DR EMBL: X82462; CA57845.1; -;  
 DR HSSP: Q07817; IMA2;  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR000712; Bcl2\_BH.

DR InterPro: IPR003093; Bcl2\_BH4.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 KW Apoptosis; Transmembrane.  
 FT NON\_TER 1  
 FT DOMAIN 120 139 BH1.  
 FT DOMAIN 171 186 BH2.  
 FT TRANSMEM 207 227 POTENTIAL.  
 SQ SEQUENCE 228 AA; 25068 MW; C499D449A585F8A9 CRC64;

Query Match 8.5%; Score 125.5; DB 1; Length 228;  
 Best Local Similarity 21.7%; Pred. No. 0.00035;  
 Matches 44; Conservative 44; Mismatches 92; Indels 23; Gaps 8;

QY 78 LDIEGFVVDYFTHRIKRGKMEWF-----GAPGLPCGVOPHEHMRVMGTIFEKKHAENFEFCQ 137  
 DB 46 LGSRALVEDLVRYKLCQRLSLVPEPSGASCAL---HSARAGDEFEERFQAISEISTQ 102  
 QY 138 LAVPRISFSLYQDVVRYTGNMOTQCPMSYGRLLIGLISFGFVAAKMMESV--ELQGV 195  
 DB 103 IHVTPGTAYARFAFEVAGSL-----FOGCVNMGRIYAFVFEFG--ALCAESYVKMKSPIL 154  
 QY 196 RNLFYVTSLFIKTRIRNNKMEHNRSDPMTLGKQMKEDYERAEAKVRKRRKRRMSMT 255  
 DB 155 PRIQDMWVITLETNLR-DWIQSNGWNGFLTL-----YGDGALIRE-ARROREGNWSL 205  
 QY 256 GAGVTAGAIQVGVVCGRMFS 278  
 DB 206 KT-VLTGAVVALGALMTVGVALFAS 227

## RESULT 10

BCL2\_MOUSE  
 ID BCL2\_MOUSE STANDARD; PRT: 236 AA.

AC P10417; P10418;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2 OR BCL-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
 RC STRAIN=BALB/C; TISSUE=Liver;  
 RX MEDLINE=87187643; PubMed=3032455;  
 RA Negri M., Sillit E., Kozak C., Tsujimoto Y., Croce C.M.;  
 RT "Molecular analysis of mbcl-2: structure and expression of the murine  
 RT gene homologous to the human gene involved in follicular lymphoma";  
 RL Cell 49:455-463(1987).  
 RN [2]  
 RP REVISIONS TO 221-222.  
 RX MEDLINE=92375724; PubMed=1508712;  
 RA Egnuch Y., Ewert D.L., Tsujimoto Y.;  
 RT "Isolation and characterization of the chicken bcl-2 gene: expression  
 RT in a variety of tissues including lymphoid and neuronal organs in  
 RT adult and embryo";  
 RL Nucleic Acids Res. 20:4187-4192(1992).  
 RN [3]  
 RP PHOSPHORYLATION BY PKC, AND MUTAGENESIS OF SERINE RESIDUES.  
 RX MEDLINE=97277291; PubMed=9115213;  
 RA Ito T., Deng X., Carr B., May W.S., Jr.;  
 RT "Bcl-2 phosphorylation required for anti-apoptosis function.";  
 RL J. Biol. Chem. 272:11671-11673(1997).  
 RN [4]  
 RP DEPHOSPHORYLATION BY PP2A.

RX MEDLINE:99069407; PubMed:9852076;  
 RA Deng X., Ito T., Carr B., Mundy M., May W.S. Jr.;  
 RT "Reversible phosphorylation of Bcl2 following interleukin 3 or  
 RT bryostatin 1 is mediated by direct interaction with protein  
 RT phosphatase 2A\*";  
 RL J. Biol. Chem. 273:34157-34163(1998).  
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 CC including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 CC permeability. Appears to function in a feedback loop system with  
 CC caspases. Inhibits caspase activity either by preventing the  
 CC release of cytochrome c from the mitochondria and/or by binding to  
 CC the apoptosis-activating factor (APAF-1).  
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2  
 CC domains, and is necessary for anti-apoptotic activity (By  
 CC similarity). Also interacts with APAF-1 and RAIF-1.  
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
 CC membrane of the nuclear envelope and the endoplasmic reticulum.  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta;  
 CC are produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues.  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and  
 CC for interaction with RAIF-1.  
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
 CC anti-apoptotic activity. Growth factor-stimulated phosphorylation  
 CC on Ser-70 by PKC is required for the anti-apoptosis activity and  
 CC occurs during the G2/M phase of the cell cycle. In the absence of  
 CC growth factors, Bcl2 appears to be phosphorylated by other protein  
 CC kinases such as ERKs and stress-activated kinases.  
 CC Dephosphorylated by protein phosphatase 2A (PP2A).  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The  
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic  
 CC activity, causes the release of cytochrome c into the cytosol  
 CC promoting further caspase activity.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: L31532; AAA37282.1; -;  
 DR EMBL: M16506; AAA37282.1; JOINED.  
 DR EMBL: M16506; AAA37281.1; -;  
 DR PIR: A25960; TVMSA1.  
 DR PIR: B25960; TVMSA1.  
 DR PIR: E37332; E37332.  
 DR HSP: 007817; 1MAZ.  
 DR MGD: MGI:88138; Bcl2.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR003093; BCL2\_BH4.  
 DR InterPro: IPR004725; BCL2-reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRFAMs: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS00062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4\_1; 1.  
 DR PROSITE: PS01260; BH4\_2; 1.  
 DR PROSITE: PS00663; BH4\_2; 1.  
 KW Apoptosis; Alternative splicing; Transmembrane; Mitochondrion;

KW Phosphorylation.  
 FT DOMAIN 10 30 BH4.  
 FT DOMAIN 90 104 BH3.  
 FT DOMAIN 133 152 BH1.  
 FT DOMAIN 184 199 BH2.  
 FT TRANSMEM 209 230 POTENTIAL.  
 FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).  
 FT MOD\_RES 70 70 PHOSPHORYLATION (BY PKC).  
 FT VARSLIC 193 236 DAFELYGSPMRPDEFSLSKLTLSALVAGCTTCAYL  
 FT VARSLIC 193 236 GKK -> VGACTIVE (IN ISOFORM BETA).  
 SQ SEQUENCE 236 AA; 26425 MW; AAB5EF6B076BE0A CRC64;  
 Query Match 8.0%; Score 118.5; DB 1; Length 236;  
 Best Local Similarity 20.0%; Pred. No. 0.0016;  
 Matches 49; Conservative 40; Mismatches 73; Indels 83; Gaps 11;  
 QY 79 DIEGFVVDYFTHIRONGMEW-----FGA---PGLPCGVDP----- 112  
 DB 10 DNREIVMKYHYKLSORGYEMDAGDADAPLGAAPPGI-FSFQPSNDMPAVHREMAR 68  
 QY 113 -----HEMRYMGTFEFKKHAFNFTFCQLAVPRISFLYQ 150  
 DB 69 TSPRLPLVATAGALSPVPCVHLTLRRAGDDPSRRYRRDPFAMSSQLHFTTARGRA 128  
 QY 151 DVYRTVGNAGTDCPSYGRILGLISGGRVAAKMEV--ELGGVRNLVYVTSLEFT 208  
 DB 129 TVVE-----ELFRDGVNMGWIVAFEEGGVMC---VESVNRKSPVDNALMTEYLR 180  
 QY 209 RIRNNKEHNRSDDEMTL-GKQMKEDYERAEKVGRRKQNRW-----SMIGAG 258  
 DB 181 HL-HTWIQDNGMDAVELVGPSPRPLDFPS-----WLSLKLTLSLALVGC 226  
 QY 259 VTAGA 263  
 DB 227 ITLGA 231  
 RESULT 11  
 BCL2\_BOVIN  
 ID BCL2\_BOVIN STANDARD; PRT; 229 AA.  
 AC 002718;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Holstein; TISSUE=thymus;  
 RA Reyes R.A., Cockrell G.L.;  
 RT "Bovine leukemia virus associated-leukemogenesis is correlated  
 RT with suppression of programmed cell death and increased expression  
 RT of Bcl-2";  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 CC including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 CC permeability. Appears to function in a feedback loop system with  
 CC caspases. Inhibits caspase activity either by preventing the  
 CC release of cytochrome c from the mitochondria and/or by binding to  
 CC the apoptosis-activating factor (APAF-1) (By similarity).  
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2  
 CC domains, and is necessary for anti-apoptotic activity (By  
 CC similarity). Also interacts with APAF-1 and RAIF-1 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
 CC membrane of the nuclear envelope and the endoplasmic reticulum (By  
 CC similarity).





FT	DOMAIN	10	30	BH4
FT <td>DOMAIN</td> <td>93</td> <td>107</td> <td>BH3.</td>	DOMAIN	93	107	BH3.
FT <td>DOMAIN</td> <td>136</td> <td>155</td> <td>BH1.</td>	DOMAIN	136	155	BH1.
FT <td>DOMAIN</td> <td>187</td> <td>202</td> <td>BH2.</td>	DOMAIN	187	202	BH2.
FT <td>TRANSMEM</td> <td>212</td> <td>233</td> <td>POTENTIAL.</td>	TRANSMEM	212	233	POTENTIAL.
FT <td>SITE</td> <td>34</td> <td>35</td> <td>CLEAVAGE (BY CASPASE-3).</td>	SITE	34	35	CLEAVAGE (BY CASPASE-3).
FT <td>MOD_RES</td> <td>70</td> <td>70</td> <td>PHOSPHORYLATION (BY PKC) (BY SIMILARITY).</td>	MOD_RES	70	70	PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
FT <td>VARSPDIC</td> <td>196</td> <td>239</td> <td>DAPELVGSGMRPLRPFSLSKTLSTLALVACITLGNVL</td>	VARSPDIC	196	239	DAPELVGSGMRPLRPFSLSKTLSTLALVACITLGNVL
FT <td></td> <td></td> <td></td> <td>GHK -&gt; VASGSD8 (IN ISOFORM BETA).</td>				GHK -> VASGSD8 (IN ISOFORM BETA).
FT <td>VARIANT</td> <td>7</td> <td>7</td> <td>T -&gt; S.</td>	VARIANT	7	7	T -> S.
FT <td></td> <td></td> <td></td> <td>/FTID=VAR_000827.</td>				/FTID=VAR_000827.
FT <td>VARIANT</td> <td>59</td> <td>59</td> <td>P -&gt; S (IN NON-HODGKINS-LYMPHOMA; SOMATIC</td>	VARIANT	59	59	P -> S (IN NON-HODGKINS-LYMPHOMA; SOMATIC
FT <td></td> <td></td> <td></td> <td>MUTATION).</td>				MUTATION).
FT <td>VARIANT</td> <td>93</td> <td>93</td> <td>V -&gt; I (IN NON-HODGKINS-LYMPHOMA; SOMATIC</td>	VARIANT	93	93	V -> I (IN NON-HODGKINS-LYMPHOMA; SOMATIC
FT <td></td> <td></td> <td></td> <td>MUTATION).</td>				MUTATION).
FT <td></td> <td></td> <td></td> <td>/FTID=VAR_000828.</td>				/FTID=VAR_000828.
FT <td>MUTAGEN</td> <td>34</td> <td>34</td> <td>D-&gt;A: ABOLISHES CLEAVAGE BY CASPASE-3.</td>	MUTAGEN	34	34	D->A: ABOLISHES CLEAVAGE BY CASPASE-3.
FT <td>MUTAGEN</td> <td>64</td> <td>64</td> <td>D-&gt;A: NO EFFECT ON CLEAVAGE BY CASPASE-3.</td>	MUTAGEN	64	64	D->A: NO EFFECT ON CLEAVAGE BY CASPASE-3.
FT <td>MUTAGEN</td> <td>145</td> <td>145</td> <td>G-&gt;A: NO HETERODIMERIZATION WITH BAX AND</td>	MUTAGEN	145	145	G->A: NO HETERODIMERIZATION WITH BAX AND
FT <td></td> <td></td> <td></td> <td>LOSS OF ANTI-APOPTOTIC ACTIVITY.</td>				LOSS OF ANTI-APOPTOTIC ACTIVITY.
FT <td>MUTAGEN</td> <td>188</td> <td>188</td> <td>W-&gt;A: NO HETERODIMERIZATION WITH BAX AND</td>	MUTAGEN	188	188	W->A: NO HETERODIMERIZATION WITH BAX AND
FT <td></td> <td></td> <td></td> <td>LOSS OF ANTI-APOPTOTIC ACTIVITY.</td>				LOSS OF ANTI-APOPTOTIC ACTIVITY.
FT <td>CONFLICT</td> <td>48</td> <td>48</td> <td>I -&gt; F (IN REF. 4).</td>	CONFLICT	48	48	I -> F (IN REF. 4).
FT <td>CONFLICT</td> <td>59</td> <td>59</td> <td>P -&gt; T (IN REF. 3).</td>	CONFLICT	59	59	P -> T (IN REF. 3).
FT <td>CONFLICT</td> <td>117</td> <td>117</td> <td>S -&gt; R (IN REF. 3).</td>	CONFLICT	117	117	S -> R (IN REF. 3).
FT <td>CONFLICT</td> <td>129</td> <td>129</td> <td>R -&gt; C (IN REF. 4).</td>	CONFLICT	129	129	R -> C (IN REF. 4).
FT <td>SEQUENCE</td> <td>239 AA;</td> <td>26266 MW;</td> <td>3C49F2B714DC9C6B CRC64;</td>	SEQUENCE	239 AA;	26266 MW;	3C49F2B714DC9C6B CRC64;
Query Match		7.8%;	Score 116;	DB 1; Length 239;
Best Local Similarity		19.4%;	Pred. No. 0.0027;	
Matches	48;	Conservative	39;	Mismatches 76; Indels 84; Gaps 10;
QY	79	DIEGVVDYFTRIRIRONGEMF-----	100	
DB	10	DREIWMKTIHKKLSORGTEWDAGDVGAPGAAPRGIFSSQPGHTPPAASRDPAVAT	69	
QY	101	-----GAPGLFCG-----VQP-EHEEMRWKGTIFEKKHAENFEFFCEQLLAVPRISFL	148	
DB	70	SFLQTPAAPGAAGAPALSPVPVVIH.TLRQADDPSRRYRPFAMSSQLHLTPPTARCR	129	
QY	149	YQDVAVRTGNAQTDQCPMSYGRILGISGCGVYAAKKMESV--ELQGGVRYNLFVYTSLFI	206	
DB	130	FATVE-----ELFPGDGVNMGRIYAFEEFGGYWC---VESVARENSPLVDNIALMTEYL	181	
QY	207	KTRIRNNKKEHNRSWDEMTL-GKQMKEDYFAEAEKVRKRNRR-----SMIG	256	
DB	182	NRHL-HTWIDQNGWDALFVLYGPMRPLDPS-----WLSLKTLLSLALVG	227	
QY	257	AGVTAGA	263	
DB	228	ACTTLGA	234	
RESULT 14				
BCL2_RAT	ID	BCL2_RAT	STANDARD;	PRT; 236 AA.
AC	P49950;	062837;	Q64032;	
DT	01-OCT-1996	(Rel. 34,	Created)	
DT	01-NOV-1997	(Rel. 35,	Last sequence update)	
DT	15-JUN-2002	(Rel. 41,	Last annotation update)	
DE	Apoptosis regulator Bcl-2.			
GN	BCL2 OR BCL-2.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eultheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
FX	MEDLINE=94193015; PubMed=8144041;			
TA	Sato T., Irie S., Krajewski S., Reed J.C.;			
	Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein. "			

RL Gene 140:291-292(1994).  
 RP [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Sprague-Dawley: TISSUE-Ovary;  
 RX MEDLINE=95129487; PubMed=7828536;  
 RA Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;  
 RT "Expression of members of the bcl-2 gene family in the immature rat  
 RT ovary: equine chorionic gonadotropin-mediated inhibition of granulosa  
 RT cell apoptosis is associated with decreased bax and constitutive  
 RT bcl-2 and bcl-x-long messenger ribonucleic acid levels.";  
 RL Endocrinology 136:232-241(1995).  
 RL [3]  
 RP SEQUENCE OF 19-172 FROM N.A.  
 RX MEDLINE=95059917; PubMed=7969891;  
 RA Castren E., Ohga Y., Berzaghi M.P., Tzimagiorgis G., Thoenen H.,  
 RA Lindholm D.;  
 RT "bcl-2 messenger RNA is localized in neurons of the developing and  
 RT adult rat brain.";  
 RL Neuroscience 61:165-177(1994).  
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 CC including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 CC permeability. Appears to function in a feedback loop system with  
 CC caspases. Inhibits caspase activity either by preventing the  
 CC release of cytochrome c from the mitochondria and/or by binding to  
 CC the apoptosis-activating factor (APAF-1).  
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 CC Bcl-x(L). Heterodimerization with BAX requires intact BHL and BH2  
 CC domains, and is necessary for anti-apoptotic activity (By  
 CC similarity). Also interacts with APAF-1 and RAIF-1 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
 CC membrane of the nuclear envelope and the endoplasmic reticulum.  
 CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues, with  
 CC highest levels in reproductive tissues. In the adult brain,  
 CC expression is localized in mitral cells of the olfactory bulb,  
 CC granule and pyramidal neurons of hippocampus, pontine nuclei,  
 CC cerebellar granule neurons, and in ependymal cells. In prenatal  
 CC brain, expression is higher and localized in the neuroepithelium  
 CC and in the cortical plate.  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and  
 CC for interaction with RAIF-1 (By similarity).  
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
 CC anti-apoptotic activity. Growth factor-stimulated phosphorylation  
 CC on Ser-70 by PKC is required for the anti-apoptosis activity and  
 CC occurs during the G2/M phase of the cell cycle. In the absence of  
 CC growth factors, Bcl2 appears to be phosphorylated by other protein  
 CC kinases such as ERKs and stress-activated kinases.  
 CC -1- PTM: Proteolytically cleaved by caspases 2A (PP2A) (By similarity).  
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic  
 CC activity, causes the release of cytochrome c into the cytosol  
 CC promoting further caspase activity (By similarity).  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
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 CC -----  
 DR EMBL: L14680; AAA53662.1; -;  
 DR EMBL: U34964; AAAT7687.1; -;  
 DR EMBL: S74122; -; NOT\_ANNOTATED\_CDS.  
 DR HSSP: 007817; 1MAZ.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR00712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH4.

DR InterPro: IPR004725; Bcl2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRFAMs: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS0062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4; 1.  
 DR PROSITE: PS0063; BH4\_2; 1.  
 DR Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.  
 KW Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.  
 FT DOMAIN 10 30  
 FT DOMAIN 90 104 BH3.  
 FT DOMAIN 133 152 BH1.  
 FT DOMAIN 184 199 BH2.  
 FT TRANSMEM 209 230  
 FT SITE 34 35  
 FT MOD\_RES 70 70  
 FT CONFLICT 42 42 A -> R (IN REF. 2).  
 FT CONFLICT 157 157 S -> G (IN REF. 1).  
 FT CONFLICT 164 164 S -> Y (IN REF. 2).  
 FT CONFLICT 212 212 L -> Q (IN REF. 2).  
 SQ SEQUENCE 236 AA; 26622 MW; E7688CB9071A872A CRC64;  
 Query Match 7.7%; Score 114.5; DB 1; Length 236;  
 Best Local Similarity 19.2%; Pred. No. 0.0036; Indels 83; Gaps 10;  
 Matches 47; Conservative 40; Mismatches 75;  
 QY 79 DIGEVDVYDTHIRONGMEM-----FGAGLPCGYOP----- 112  
 DB 10 DNEIYWKYTHYLSQRYGEMDGDSDASPLRAAPRPGI-FSQGPSNRTPAVHRPTAAR 68  
 QY 113 -----HEMMRWGTFTEKKAHNEFTFCQLAVPRISLYQ 150  
 DB 69 TSPRLPVLAVNAGPALSPVPVHLTLRRAGDDFSRRYRDFEMSSQLHFTFARGRA 128  
 QY 151 DVRTVGNAGTDDCPMSYGRLLIGLSFGGTVAKKMEV--ELGGVRLFYTSIFIKT 208  
 DB 129 TVVE-----ELFRDGVNMGRIYAFEEFGVVC--VESVNRRESPLVDNALMTEYLNR 180  
 QY 209 RINNMKEHNRSDDMPTL-GKQMKEDYERAEKVRKQRNRR-----SMIGAG 258  
 DB 181 HL-HTWQDNGMDARVVELGSPMRPLFDS-----WLSKTLTSLALVGC 226  
 QY 259 VTAGA 263  
 DB 227 ITLGA 231  
 RESULT 15  
 BCLX\_CHICK STANDARD: PRT; 229 AA.  
 ID BCLX\_CHICK  
 AC Q07816; Q98908;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-X.  
 GN BCL2L1 OR BCLX OR BCL-X.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RX SEQUENCE FROM N.A. (SHORT FORM).  
 RX MEDLINE=93364977; PubMed=8358789;  
 RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,  
 RA Turka L.A., Mao X., Nunez G., Thompson C.B.;  
 RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator  
 RT of apoptotic cell death.";  
 RL Cell 74:597-608(1993).







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OM protein - protein search, using sw model

Run on: February 24, 2003, 11:51:59 ; Search time 33 seconds

(without alignments)  
1748.279 Million cell updates/sec

Title: US-09-993-420A-3  
Perfect score: 1479  
Sequence: 1 MRCGTADNLTNPAYRRRTM.....AGATGCVVCGRMFSLK 280

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21: \*  
1: sp.\_archaea: \*  
2: sp.\_bacteria: \*  
3: sp.\_fungi: \*  
4: sp.\_human: \*  
5: sp.\_invertebrate: \*  
6: sp.\_mammal: \*  
7: sp.\_mhc: \*  
8: sp.\_organelle: \*  
9: sp.\_phage: \*  
10: sp.\_plant: \*  
11: sp.\_rodent: \*  
12: sp.\_virus: \*  
13: sp.\_vertebrate: \*  
14: sp.\_unclassified: \*  
15: sp.\_vivirus: \*  
16: sp.\_bacteriophage: \*  
17: sp.\_archaeo: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	151	10.2	193	11	088996
2	139	9.4	233	6	088996
3	136	9.2	233	6	088996
4	134	9.1	233	6	09MTW4
5	132	8.9	233	6	09N1A2
6	130	8.8	233	6	09M2S7
7	124.5	8.4	233	11	035844
8	124.5	8.4	217	11	09CWM5
9	124	8.4	180	6	09BD5
10	124	8.4	180	6	09BD5
11	117.5	7.9	238	13	090298
12	110.5	7.5	236	11	0923R6
13	108	7.3	1329	16	08YVT7
14	99	6.7	177	13	0902N1
15	99	6.7	188	4	09H1R6
16	99	6.7	331	11	P97287

17	98	6.6	330	11	0921P3
18	96.5	6.5	757	16	0914S8
19	96	6.5	188	11	090WX2
20	96	6.5	235	11	035843
21	95	6.4	350	4	09UNJ1
22	93	6.3	176	13	08UWD5
23	91.5	6.2	463	5	09N960
24	91.5	6.2	639	10	09PLA9
25	90.5	6.1	279	16	08X369
26	90.5	6.1	644	16	08UC9
27	89.5	6.1	211	13	09W6F1
28	89	6.0	101	11	09CR14
29	88.5	6.0	219	11	099N36
30	88.5	6.0	283	16	08X3U5
31	88	5.9	255	13	0919N3
32	87.5	5.9	104	11	09R289
33	87.5	5.9	152	6	09SKR3
34	86	5.8	326	17	08T1P1
35	86	5.8	184	16	09CF9A
36	85.5	5.8	961	16	08R608
37	85	5.7	1353	4	09Y4B5
38	85	5.7	2368	2	093TW6
39	85	5.7	2904	11	09EPN0
40	85	5.7	2931	11	09EPN9
41	85	5.7	2936	11	09EPN1
42	84.5	5.7	150	16	09P87
43	84.5	5.7	430	16	09HXP6
44	84.5	5.7	559	5	09NG26
45	84.5	5.7	568	5	09VEB6

## ALIGNMENTS

RESULT 1	ID	088996	PRELIMINARY;	PRT;	193 AA.
AC	088996;				
DT	01-NOV-1998 (TREMBLrel. 08, Created)				
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)				
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
DE	Bcl-w.				
GN	BCL-W.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;				
RX	MEDLINE=99292146; PubMed=10366024;				
RA	Hammer S., Skoglova Y., Lindholm D.;				
RT	"Differential expression of bcl-w and bcl-x messenger RNA in the				
RT	developing and adult rat nervous system.";				
RL	Neuroscience 91:673-684(1999).				
DR	EMBL: AF096291; AAC64200.1; -				
DR	HSSP: O07817; IMZ.				
DR	InterPro: IPR000712; BCL2_BH.				
DR	InterPro: IPR003093; BCL2_BH4.				
DR	InterPro: IPR002475; BCL2_Family.				
DR	Pfam: PF00452; Bcl-2; 1.				
DR	Pfam: PF02180; BCL; 1.				
DR	SMART: SM00337; BCL; 1.				
DR	SMART: SM00265; BH4; 1.				
DR	PROSITE: PS50062; BCL2_FAMILY; 1.				
DR	PROSITE: PS01080; BH1; 1.				
DR	PROSITE: PS01258; BH2; 1.				
DR	PROSITE: PS01260; BH4; 1.				
DR	PROSITE: PS50063; BH4_2; 1.				
DR	SEQUENCE 193 AA; 20820 MW; 36D6742F4529AFB4 CRC64;				
SO	SEQUENCE				
Query Match	10.2%;	Score 151;	DB 11;	Length 193;	
Best Local Similarity	24.3%;	Pred. No. 1.8e-06;			

Matches	51: Conservative	31: Mismatches	92: Indels	36: Gaps	8:
QY	79	DIEGCVVYDFTHIRIQNGMENGAGCLGCGVGPPEHEHMRVMTQITFEKKIAENFEFFCEDL	138		
Db	9	DTRALVAIDFVGKIRKQKGYCCAGGEGPADPLIQAMRAADGETETRRRTFSDLAAL	68		
QY	139	LAVP-----RISFSLYQDVVFTVGNAAQTFDQCPSMYGRLIGLISFGGFAVAKMM--ES	188		
Db	69	HYTPSSAQQRRFTQVSDDELFGQ-----GPNMGRLVAFFVFYGAALCAESVKNKM	115		
QY	189	VELQGVRRNLEFYTSLFIKTRIRNNWKEHNRSMDPMTILGKQKEDYEAEAEKKYGRKQ	248		
Db	116	EPLVQGVQDMMV---TYLETIRLA-DWIHSSGGWAEEFTAL-----YDGALEE-ARRLR	163		
QY	249	NRNRSMIGAGVTAIGIAGVGVCCRRMPS	278		
Db	164	EGNMASVRT-VLTGAVALGALVTVAFAFRS	192		

RESULT 2	08SQ42	PRELIMINARY;	PRT;	233 AA.
ID	08SQ42			
AC	08SQ42			
DT	01-JUN-2002 (TREMblrel_21, Created)			
DT	01-JUN-2002 (TREMblrel_21, Last sequence update)			
DT	01-JUN-2002 (TREMblrel_21, Last annotation update)			
DE	Bcl-X1 protein.			
GN	BCL-XL.			
OS	Felis silvestris catus (Cat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.			
OX	NCBI_TaxId=9685;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Nagatuchi S., Sano J., Kano R., Hasegawa A.;			
RT	"Molecular cloning of feline Bcl-2 family.";			
RL	Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.			
EQ	EMBL: AB080951; BAB85656.2; -;			
SO	SEQUENCE_233 AA; 2601 MW; CD17F24FE9DA7BC9 CRC64;			

Query Match	9.4%;	Score 139;	DB 6;	Length 233;
Best Local Similarity	21.3%;	Pred. No. 3.3e-05;		
Matches	53;	Conservative	39;	Mismatches 81;
				Indels 76;
				Gaps 10

```

0Y      VDYDTHHTRONGMWF-----GAPCLPGVOPHE-----114
        ||| : ||| : | | | | | | | | | | | | | | | | | |
Db      9 VYDFLSTYLQKGYMSRFDVEENRTREARPGTSEMETPSAINGNSWHLADSPAYNGA 68

0Y      -----MARVGTTFEKKHAENFTPEOOLLAVPRISFSLYODVR 154
        : | : | : | : | : | : | : | : | : | : | : | : |
Db      69 TGHSSLDAREVIPIMAAKQAIREAGDEFFELRYRAAFSDLTSQLHTTPGTAYSOFEEGVN 128

0Y      155 TYGNNOTDOCPYSYGRLLGLLSFGFVPAKKMESV--ELOGOVENTLPVTSLFKTRIRN 212
        : | : | : | : | : | : | : | : | : | : | : | : |
Db      129 -----ELERDGYNNCRITAEFSFG--ALCEVSVDKEMOVLYSRIAMMATIYNIDL-E 179

0Y      213 NKEHNRSMDPFMLTGKOMKEDY-ERAFAEKVGRRKNRRMSMTIGAVTAGAIGIVGVV 271
        : | : | : | : | : | : | : | : | : | : | : | : |
Db      180 PWIOENGWDTEFVEL-----YGNNAAAESRKQOERSNFWLTG-----MTVAQVVL 225

0Y      272 CGRMMEFLX 280
        | : | | |
Db      226 LG-SLESRK 233

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RESULT 3	
Q9MYW4	
ID	Q9MYW4
AC	Q9MYW4
DT	01-OCT-2000
DT	01-OCT-2000
DT	01-JUN-2002
DE	Bcl-X.
	PRELIMINARY;
	PRT; 233 AA.
	Created (15, 15, Last sequence update)
	(15, 15, Last annotation update)
	(15, 21, Last annotation update)
	Bcl-X.

OS Oryctolagus cuniculus (Rabbit).  
 OS Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Knott J.C., Robertson L., James E.R.;  
 RT "Rabbit Bcl-X";  
 RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.  
 DB EMBL; AY005131; AAF86137.1; -.  
 DR HSSP; P53563; IAF3.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR003093; Bcl2\_BH4.  
 DR InterPro; IPR002475; Bcl2\_family.  
 DR InterPro; IPR004725; Bcl2\_reg.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR Pfam; PF02180; BH4; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR SMART; SM00265; BH4; 1.  
 DR TIGRFAMS; TIGR00865; bcl-2; 1.  
 DR PROSITE; PSS0062; BCL2\_FAMILY; 1.  
 DR PROSITE; PSS0180; BH1; 1.  
 DR PROSITE; PSS01258; BH2; 1.  
 DR PROSITE; PSS01259; BH3; 1.  
 DR PROSITE; PSS01260; BH4.1; 1.  
 DR PROSITE; PSS0063; BH4.2; 1.  
 SO SEQUENCE 233 AA; 25986 MW; 12DF30344AD53F93 CRC64;

Query Match	Score	DB	Length
9.28;	136;	6;	233;

Best Local Similarity 21.38; Pred. No. 6.4e-05;  
Matches 53; Conservative 38; Mismatches 82; Indels 76; Gaps 10;

[illegible]

ID	Q9N1A2	PRELIMINARY;	PRT;	233 AA.
AC	Q9N1A2;			
DF	01-OCT-2000 (TREMblrel. 15, Created)			
DF	01-OCT-2000 (TREMblrel. 15, last sequence update)			
DT	01-JUN-2002 (TREMblrel. 21, last annotation update)			
DE	Anti-apoptotic regulator Bcl-XL.			
GN	Bcl-XL.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=HEART;			
RA	Lee T. L., Canty J. M.;			
RT	"PCR Cloning of a Porcine bcl-xl cDNA from Heart."			
RL	Submitted (DNC-1999) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AF216205; AAF33212.1; -			

[illegible]

DR	PROSITE: PS50062; BCL2_FAMILY; 1.
DR	PROSITE: PS01080; BH1; 1.
DR	PROSITE: PS01258; BH2; 1.
DR	PROSITE: PS01259; BH3; 1.
DR	PROSITE: PS01260; BH4_1; 1.
DR	PROSITE: PS50063; BH4_2; 1.
DR	SEQUENCE 233 AA; 26134 MW; 012BFA1382762915 CRC64;
SO	SEQUENCE 233 AA; 26033 MW; 3083F2D8327E072E CRC64;

Query Match	8.9%;	Score 132;	DB 6;	Length 233;
Best Local Similarity	21.1%;	Pred. No. 0.00015;		
Matches 53;	Conservative 40;	Mismatches 78;	Indels 80;	Gaps 11;

Qy	84	VVDYFTHRRKRGGMENP-----GA 102
Db	9	VVDFLSYKLKSGKGYWSQSFSDVENRTEAPECTESDMETPSAINGNPSMHLADSPAUNG 68
Qy	103	PG-----LPCGVOPHEHMRVMYGTIFEKKHAENFEFCQDLAVPRISFLYQDV 152
Db	69	TGHSNSLDAREIP--MAAVKQALENAGEFEFLRRRAFSDLTSQLHTPGTAQYSEFV 126
Qy	153	VRFGVNAQTQCPMSYGRLLIGLISFGGEVYAAKMESV--ELQGYVRNLFEVTSLFIKTRI 210
Db	127	VN-----ELFRDGVNMGRIVAFFSEGG--ALCVESVDKEMQVLVSRIATMATYLIIDLH 178
Qy	211	RNNMKENHNSWDPEFTLQGMKEDI-ERRAEAKVGRKRONRQMSMIGAVTGAIGYGV 269
Db	179	EPWTDIOENGMDTFEVL-----YGNNAAEASRKQGERENFWFLTG-----MTVAGV 223
Qy	270	VYCGRMFSLK 280
Db	224	VLLG-SLFSRK 233

RESULT 6				
ID	035844	PRELIMINARY;	PRT;	233 AA.
AC	035844;			
DT	01-JAN-1998	(TREMBLrel. 05, Created)		
DT	01-JAN-1998	(TREMBLrel. 05, Last sequence update)		
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)		
DE	Bcl1-XL.			
GN	BCL2L.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
NCBI_Taxid	10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=B6/CBA; TISSUE=THYMUS;			
RX	MEDLINE=98051053; PubMed=9390687;			
RA	Yang X.-F., Weber G.F., Cantor H.;			
RT	"A novel Bcl-x isoform connected to the T cell receptor regulates			
RT	apoptosis in T cells."			
RRL	Immunity 7:629-639(1997).			
DR	EMBL; U51278; AAC53459.1; -.			
DR	HSSP; P53563; IAF3.			
DR	MGD; MGI:88139; Bcl2l.			
DR	InterPro: IPR000712; Bcl2_BH.			
DR	InterPro: IPR003093; Bcl2_BH4.			
DR	InterPro: IPR002475; Bcl2_family.			
DR	InterPro: IPR004725; Bcl2_reg.			
DR	Pfam; PF00452; Bcl-2; 1.			
DR	Pfam; PF02180; BH4; 1.			
DR	SMART; SM00265; BCL; 1.			
DR	SMART; SM00265; BH4; 1.			
DR	TIGRFAMs; TIGR00865; bcl-2; 1.			
DR	PROSITE; PS50062; BCL2_FAMILY; 1.			
DR	PROSITE; PS01080; BH1; 1.			
DR	PROSITE; PS01258; BH2; 1.			
DR	PROSITE; PS01259; BH3; 1.			
DR	PROSITE; PS01260; BH4_1; 1.			
DR	PROSITE; PS50063; BH4_2; 1.			
DR	SEQUENCE 233 AA; 26033 MW; 3083F2D8327E072E CRC64;			



Db 179 ---YGNNAAESRKGOERFNWFLTG-----MTVAGVLLG-SLFSRK 217

RESULT 9

Q9BBD5 PRELIMINARY; PRT; 180 AA.

AC Q9BBD5; 01-JUN-2001 (Tremblrel. 17, Created)

DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)

DE Anti-apoptotic regulator Bcl-XL (Fragment).

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.

NCBI\_TaxID=9913;

OX (1)

RP SEQUENCE FROM N.A.

RA Amills M., Bouzat J.;

RT "Characterization of the bovine bcl-xl gene and related pseudogenes."

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF245488; AAK31307.1; -

DR EMBL: AF245489; AAK31308.1; -

DR HSSP: Q07817; IMAZ.

DR InterPro: IPR000712; Bcl2\_BH.

DR Pfam: PF00452; Bcl-2; 1.

DR SMART: SM00337; BCL1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR PROSITE: PS01080; BH1; 1.

DR PROSITE: PS01258; BH2; 1.

DR PROSITE: PS01259; BH3; 1.

FT NON\_TER 1 180

SQ SEQUENCE 180 AA; 20062 MW; 95DC436F95DABDA6 CRC64;

Query Match 8.4%; Score 124; DB 6; Length 180;

Best Local Similarity 24.2%; Pred. No. 0.00064;

Matches 40; Conservative 33; Mismatches 66; Indels 26; Gaps 7;

QY 114 EMNRVAGCTIEKKHAENFEFCQQLAVPRISFLYQDVYRTYGNACTOCPMSTYRLIG 173

Db 38 QALREAGDEFEELRYRAFSDLTSQHLITPGTAYQSEOVVN-----ELFRDGVNMGRIYA 92

QY 174 LISFGFVAAKMMESV--ELQGVRLNFVYTSLEFKTRIRNNKKEHNRSMIDPMFLTKGM 231

Db 93 FFESEGG---ALCVESYDKEMQVLYSRITATMYATYLDHL-EPMTQENGMDTFVEL----- 144

QY 232 KEDY-ERAEAEKVKRRKONRSMIGAGYTAGAIGVGVVCGRM 275

Db 145 ---YGNNAAESRKGOERFNWFLTG-----MTVAGVLLGSL 179

RESULT 10

Q9BOX7 PRELIMINARY; PRT; 180 AA.

AC Q9BOX7; 01-JUN-2001 (Tremblrel. 17, Created)

DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)

DE Anti-apoptotic regulator Bcl-XL (Fragment).

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.

NCBI\_TaxID=9913;

OX (1)

RP SEQUENCE FROM N.A.

RA Amills M., Bouzat J.;

RT "Characterization of the bovine bcl-xl gene and related pseudogenes."

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF245487; AAK31306.1; -

DR HSSP: Q07817; IMAZ.

DR InterPro: IPR000712; Bcl2\_BH.

DR InterPro: IPR002475; BCL2\_family.

DR Pfam: PF00452; Bcl-2; 1.

DR SMART: SM00337; BCL1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR PROSITE: PS01258; BH2; 1.

DR PROSITE: PS01259; BH3; 1.

FT NON\_TER 1 180

SQ SEQUENCE 180 AA; 20056 MW; 62C4C0BD055A9EF CRC64;

Query Match 8.4%; Score 124; DB 6; Length 180;

Best Local Similarity 23.9%; Pred. No. 0.00064;

Matches 45; Conservative 35; Mismatches 70; Indels 38; Gaps 9;

QY 101 GARG-----LPCGVQPEHEMMRWGTFIEKKHAENFEFCQQLAVPRISFLYQ 150

Db 17 GAPGSRSSDAREVIP--MAAVKQALREAGDEFEELRYRAFSDLTSQHLITPGTAYQSE 74

QY 151 DVFRVGNACTOCPMSTYRLIGLISFGFVAAKMMESV--ELQGVRLNFVYTSLEFKT 208

Db 75 QVYN-----ELFRDGVNMGRIYASFSG---ALCVESYDKEMQVLYSRITATMYATYLD 126

QY 209 RIRNNKKEHNRSMIDPMFLTKGMKEDY-ERAEAEKVKRRKONRSMIGAGYTAGAIGIV 267

Db 127 HL-EPWIDENGMDTFVEL-----YGNNAAESRKGOERFNWFLTG-----MTVA 171

QY 268 GVVVCGRM 275

Db 172 GVLLGSL 179

RESULT 11

Q90298 PRELIMINARY; PRT; 238 AA.

AC Q90298; 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)

OS Brachydanio rerio (Zebrafish) (Zebra danio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

NCBI\_TaxID=7955;

OX (1)

RP SEQUENCE FROM N.A.

RA MEDLINE=21299061; PubMed=11406282;

RT "Cloning and characterization of zfbpl. a Bcl-XL homologue from the zebrafish, Danio rerio(1)."

RL Blochm. Biophys. Acta 1519:127-133(2001).

DR EMBL: AF317837; AAK81706.1; -

DR InterPro: IPR000712; BCL2\_BH.

DR InterPro: IPR003093; BCL2\_BH.

DR InterPro: IPR002475; BCL2\_family.

DR Pfam: PF00452; Bcl-2; 1.

DR Pfam: PF02180; BH4; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR PROSITE: PS01080; BH1; UNKNOWN\_1.

DR PROSITE: PS50063; BH4\_2; 1.

SQ SEQUENCE 238 AA; 26253 MW; 658394933EEFDB CRC64;

Query Match 7.9%; Score 117.5; DB 13; Length 238;

Best Local Similarity 23.4%; Pred. No. 0.0039;

Matches 39; Conservative 38; Mismatches 69; Indels 21; Gaps 7;

QY 108 GVPREHEMMRWGTFIEKKHAENFEFCQQLAVPRISFLYQDVYRTYGNACTOCPM 167

Db 85 GIDAVKALROSDANFEELRYRAFSDLTSQHLITPGTAYQSEFVMDV-----FRGVN 139

QY 168 YGRLIGLISFGFVAAKMMESV--ELQGVRLNFVYTSLEFKTRIRNNKKEHNRSMIDPMTL 227

Db 140 WGRIVGLFAFGALCVCEVK-EMSEPLVRIEMWTVYLDNHIQ-PWISQSGWSEPAET 197  
 QY 228 -GKQMKEDYERAEAEKVGRRKRRMSMIGAGTGAIGVGVCG 273  
 Db 198 FGKD-----AAESRKSQSESRKKM-LFAGMTL-----LTGVVVG 231

## RESULT 12

0923R6 PRELIMINARY: PRT: 236 AA.

AC 0923R6  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
 DE B-cell lymphoma protein 2.  
 GN BCL2.  
 OS Cricetus longicaudatus (long-tailed hamster) (Chinese hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Cricetulus.  
 OC NCBI\_Taxid=10030;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lai D.Z., Chen W., Wang H.T.;  
 RT "Construction of a robust CHO cell line for biopharmaceutical use."  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF040339; AAK92201.1; -  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH4.  
 DR InterPro: IPR002475; Bcl2\_family.  
 DR InterPro: IPR004725; Bcl2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR TIGRfams: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; UNKNOWN\_1.  
 DR PROSITE: PS01258; BH2; UNKNOWN\_1.  
 DR PROSITE: PS01259; BH3; UNKNOWN\_1.  
 DR PROSITE: PS01260; BH4; 1; UNKNOWN\_1.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 DR SEQUENCE 236 AA; 26500 MW; BEDF052FE32CA8B8 CRC64;

Query Match 7.5%; Score 110.5; DB 11; Length 236;  
 Best Local Similarity 19.3%; Pred. No. 0.018;

Matches 47; Conservative 41; Mismatches 73; Indels 83; Gaps 11;

QY 79 DIEGFVVDYFTHRIKQNGEM-----FGA---PGLPGVQPE----- 112  
 Db 10 DNREIVMKYIHYKLSQKGYEMDVGVDAPLGAAPTGI-FSQPESNPTPAVHRDMAR 68  
 QY 113 -----HEMRYMGTIFEKHAENFEFCQILLAVRISFSLYQ 150  
 Db 69 TSPLRPIVATTGPTLSPVPVAVHLTKRAGDPSRRYRDRDAEMSSQHLPTARGRFA 128  
 QY 151 DVYRTVGAQTDQCPMSYGRLLIGLISFGFVAARKMESV--ELQGVNLFVYTSLYKT 208  
 Db 129 TVVE-----ELFRDGVNMGRIVAFEEFGVVC---VESVNRMSPLVIALMTETYLNR 180  
 QY 209 RIRNNKKEHNSWDEFTML-GKQKEDYERAEAEKVGRRKRRM-----SMIGAG 258  
 Db 181 HL-HTWIODNGMDAFVFLYGPSVAPLFDFS-----WLSLTLLNLALVAGAC 226  
 QY 259 VTAG 262  
 Db 227 ITLG 230

## RESULT 13

08YYT7 PRELIMINARY: PRT: 1329 AA.

AC 08YYT7  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
 DE WD-repeat containing protein.  
 GN ALU0759.  
 OS Anabaena sp. (strain PCC 7120).  
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
 OC NCBI\_Taxid=103690;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21595285; PubMed=11759840;  
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,  
 RA Watanabe A., Iriuchij M., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
 RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,  
 RA Yasuda M., Tabata S.;  
 RT "Complete genomic sequence of the filamentous nitrogen-fixing  
 cyanobacterium Anabaena sp. strain PCC 7120."  
 RL DNA Res. 8:205-213(2001).  
 DR EMBL: AF003583; BAB72716.1; -  
 DR InterPro: IPR001680; WD40.  
 DR Pfam: PF00400; WD40; 15.  
 DR PRINTS: PR00320; GPROTEINBRPT.  
 DR SMART: SM00320; WD40; 16.  
 DR PROSITE: PS00678; WD\_REPEATS\_1; UNKNOWN\_7.  
 DR PROSITE: PS50082; WD\_REPEATS\_2; 5.  
 DR PROSITE: PS50294; WD\_REPEATS\_REGION; 1.  
 DR KW Complete proteome.  
 DR SEQUENCE 1329 AA; 148584 MW; 0AE2DC35BEED07359 CRC64;

Query Match 7.3%; Score 108; DB 16; Length 1329;  
 Best Local Similarity 22.7%; Pred. No. 0.33;  
 Matches 68; Conservative 39; Mismatches 101; Indels 92; Gaps 14;

QY 12 NPAYRRRTATGEMKEFLGKTEPTDFGINSADQDLPSPRQASTRR-MSIGSI--DG 68  
 Db 173 NPAYKRRLTFA-----LLGVA-----TPGDLIQDKTRTPFNIGAILDQ 211  
 QY 69 -KINDWEPRLDIEGFVVDYFTHRIKQNGEMFGAPGPCVQ----- 110  
 Db 212 FKIDIEPLAKGLAGKVEN--PQAVMOEVLAVTG--GQPLTQVCELGKALSIEKRD 267  
 QY 111 ---PEHEMRYMGTIFEKHAENFE-----TFCEQLLAVRIS---FSLYQDVYRT 155  
 Db 268 RSVDENGIIELVKEIINHQIIDNWEANDKQEHKTRIRLLISEISVALLGYQQLIQ 327  
 QY 156 VGNMQTDQCPMSYGRLLIGLISFGFVAARKMESVLEQGVNLFVYTSLEIKRIRRN- 213  
 Db 328 VEMTADSSFEQMRRLTGLV-----VQOQGLRVYNOYRNVFDLSWVENEL 374  
 QY 214 -----WKEHNSWDEFTMLGKQMKEDYERAEAEKVGRRKRRMSMIGAGVTA 261  
 Db 375 GKLRFYADKLRAWESNIDQNTCLMG-----EDLEKARVADGKRLSDVDRFLSASVEA 430

## RESULT 14

090ZNI PRELIMINARY: PRT: 177 AA.

AC 090ZNI  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
 DE Anti-apoptotic NR13.  
 GN Gallus gallus (chicken).  
 OS Gallus gallus (chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_Taxid=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Gillet G., Lalle P., Miscopein A.;  
 RT "Electrostatic interactions between Bcl-2 homology domains BH3 and BH4  
 are essential for NR13 anti-apoptotic activity."  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

Search completed: February 24, 2003, 11:54:41  
Job time : 36 secs

